



## DECLARATION

In the matter of U.S. Patent  
Application Ser. No. 10/070,387  
in the name of Naoki MIDOH, et al.

I, Kyoko IMAMURA, of Kyowa Patent and Law Office, 2-3,  
Marunouchi 3-Chome, Chiyoda-Ku, Tokyo-To, Japan, declare  
and say:

that I am thoroughly conversant with both the Japanese  
and English languages; and,

that the attached document represents a true English  
translation of Japanese Patent Application No. 2000-104291  
filed on April 6, 2000.

I further declare that all statements made herein of  
my own knowledge are true and that all statements made on  
information and belief are believed to be true; and further  
that these statements were made with the knowledge that  
willful false statements and the like so made are punishable  
by fine or imprisonment, or both, under Section 1001 of Title  
18 of the United States Code, and that such willful false  
statements may jeopardize the validity of the application  
or any patent issued thereon.

Dated: June 10, 2004

Kyoko IMAMURA  
Kyoko IMAMURA



2000-104291

Name of Document: Patent Application

Reference Number: PM1577

Application Date: April 6, 2000

To: The Commissioner of The Patent Office

International Patent Classification: C12N

Inventor:

Address: c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

Name: Naoki MIDOH

Inventor:

Address: c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

Name: Kaoru OKAKURA

Inventor:

Address: c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

Name: Koichi MIYAMOTO

Inventor:

Address: c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

Name: Manabu WATANABE

Inventor:

Address: c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

Name: Koji YANAI

**Inventor:**

**Address:** c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

**Name:** Tetsuya YASUTAKE

**Inventor:**

**Address:** c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

**Name:** Sato AIHARA

**Inventor:**

**Address:** c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

**Name:** Takafumi FUTAMURA

**Inventor:**

**Address:** c/o Technische Universitat Berlin,  
Max-Volmer-Institut fur Biophysikalische Chemie  
und Biochemie, Franklinstr. 29, D-10587 Berlin,  
Germany

**Name:** Horst Kleinkauf

**Inventor:**

**Address:** c/o Pharmaceutical Technology Labs., Meiji Seika  
Kaisha, Ltd.  
788, Kayama, Odawara-Shi, Kanagawa-Ken

**Name:** Takeshi MURAKAMI

**Applicant:**

Identification Number: 000006091

Name: MEIJI SEIKA KAISHA, LTD.

Representative: Ichiro KITAZATO

Tel.: 03-3273-3357

**Priority Claim of Earlier Application**

**Application Number: Patent Application No. 1999-253040**  
**Application Date: September 7, 1999**

**Indication of the FEE:**

**Account Number: 008305**  
**Fee: 21,000 Yen**

**List of Documents filed:**

<b>Specification</b>	<b>1 copy</b>
<b>Abstract</b>	<b>1 copy</b>
<b>Drawing</b>	<b>1 copy</b>
<b>Certificate for Entrustment</b>	<b>3 copies</b>
<b>Indication of Reference</b>	<b>-omitted-</b>

**Proofreading:** **Needed**



[Designation of Document] Specification

Title of the Invention

Cyclic depsipeptide synthetase gene

Claims

1. A gene carrying the following DNA (a) or (b):
  - (a) DNA of a nucleotide sequence shown as SQ ID No. 1;
  - (b) a microorganism-derived DNA hybridizing with the DNA of the nucleotide sequence (a) under stringent conditions and encoding a protein with cyclic depsipeptide synthetase activity.
2. A protein described below in (a) or (b):
  - (a) a protein of an amino acid sequence shown as SQ ID No. 2;
  - (b) a protein of an amino acid sequence prepared through deletion, substitution or addition of one or several amino acids in the amino acid sequence (a) and with cyclic depsipeptide synthetase activity.
3. A recombinant vector carrying a gene according to claim 1.
4. A microorganism harboring a recombinant vector according to claim 3 and expressing the gene.
5. A microorganism according to claim 4, wherein the microorganism is a fungus producing the substance PF1022.
6. A method for producing the substance PF1022 and a derivative thereof by using a microorganism according to claim 4 or 5.

Detailed Description of the Invention

[0001]

Technical Field to which the Invention Belongs

The present invention relates to the cyclic depsipeptide synthetase gene for producing the substance PF1022 as a cyclic depsipeptide with anthelmintic activity, a protein encoded by the gene, a recombinant vector using the gene, and a method for producing the substance PF1022 in a substance PF1022-producing microorganism integrated with the recombinant vector.

[0002]

Prior Art

The substance PF1022 [*cyclo(D-lactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl-D-lactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl)*]<sup>1</sup>] is the cyclic depsipeptide produced by a filamentous fungus of Agonomycetales, namely the strain PF1022 [Mycelia sterilia; the strain was deposited as FERM BP-2671 at National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Japan]. The substance PF1022 exerts an extremely high anthelmintic activity on nematodes parasitic on animals [Japanese Patent publication No. 35796/1991; Sasaki, T. et al., *J. Antibiotics.*, 45, 692 (1992)]. Therefore, the substance is useful as a anthelmintic for animals and is additionally useful as a raw material for the synthesis of a more highly active derivative of the substance.

[0003]

The amounts of secondary metabolites produced by microorganisms and separated from natural origins are generally very slight. So as to industrially utilize such metabolites, therefore, the productivity of the secondary metabolites is necessarily increased. For the increase of the productivity, the examination of the culturing methods and the culture medium

components, the modification of the fermentation conditions such as addition of the precursors, and the mutation of the strains by ultraviolet irradiation or mutagen are carried out. In recent years, the productivity has been increased by utilizing gene recombinant technology in addition to the aforementioned methods.

[0004]

As the method, the enhancement of the expression of the genes of enzymes involved in the biosynthetic pathways, the enhancement of the expression of the genes involved in the control of the biosynthesis, and blockage of unnecessary biosynthetic pathways and the like are practically effected [Khetan, A. and Hu, W.-S. Manual of Industrial Microbiology and Biotechnology 2nd edition, p. 717, (1999)]. As a specific example, further, it has been known a method for improving the productivity, comprising allowing the hemoglobin gene of a bacterium to be expressed for the purpose of the improvement of the oxygen usability [Minas, W. et al., Biotechnol. Prog. 14, 561, (1998)].

[0005]

The most general means for the improvement of the productivity by gene recombinant technology is the enhancement of the expression of the genes of enzymes involved in biosynthetic pathway. For the application of the means, essentially, the transformation method of a subject microorganism is established; a promoter and a terminator applicable to the enhancement of the expression are to be present; and the biosynthetic pathway is to be elucidated and their genes are to be isolated. The transformation method of a fungus producing the substance PF1022, comprising integrating

a foreign gene, has already been established (WO 97/00944); and also, a report concerning the promoter and terminator applicable to the enhancement of the expression has been issued (Japanese Patent Application No. 252851/1999). However, no gene involved in the biosynthetic pathway has been isolated.

[0006]

The substance PF1022 is of a structure comprising L-N-methylleucine, D-lactic acid, and D-phenyllactic acid, which are bonded together through ester bonds and amide bonds. It is considered that the substance is synthesized from 4 molecules of L-leucine, 2 molecules of D-lactic acid and 2 molecules of D-phenyllactic acid by a certain peptide synthetase in a fungus producing the substance. Peptide synthetase means an enzyme involved in the biosynthesis of microbial secondary metabolites, such as peptide, depsipeptide, lipopeptide and peptide lactone, from substrates of amino acids and hydroxy acid. The sequences of some peptide synthetases have already been elucidated [Marahiel, M. A. et al., Chem. Rev., 97, 2651, (1997)]. The reaction with such enzyme is totally different from the synthetic system of protein with ribosome using mRNA as template. Peptide synthetase has one domain for each substrate, where each substrate is activated with ATP for binding through phosphopantothenic acid in the domain; and the resulting bound substrates form amide bonds or ester bonds due to the catalytic actions in the regions between the individual domains.

[0007]

Problems that the Invention is to Solve

The cyclic depsipeptide synthetase gene capable of improving the productivity of the substance PF1022 is provided, by permitting excess expression thereof in a fungus producing

the substance PF1022.

[0008]

#### Means for Solving the Problems

So as to overcome the problem, the inventors isolated the cyclic depsipeptide synthetase gene for the synthesis of the substance PF1022 from a fungus producing the substance PF1022, on the basis of the sequence of the conserved region of a known peptide synthetase. Furthermore, the inventors successfully improved the productivity of the substance PF1022 by preparing an expression vector modified with the promoter and terminator of the gene and integrating the expression vector in the fungus producing the substance PF1022. Thus, the invention has been achieved.

[0009]

More specifically, the invention relates to the following aspects.

1. A gene carrying the following DNA (a) or (b):

(a) DNA of a nucleotide sequence shown as SQ ID No. 1;  
(b) a microorganism-derived DNA hybridizing with the DNA of the nucleotide sequence (a) under stringent conditions and encoding a protein with cyclic depsipeptide synthetase activity.

2. A protein described below in (a) or (b):

(a) a protein of an amino acid sequence shown as SQ ID No. 2;  
(b) a protein of an amino acid sequence prepared by deletion, substitution or addition of one or several amino acids in the amino acid sequence (a) and with cyclic depsipeptide synthetase activity.

3. A recombinant vector carrying a gene in a first aspect

of the invention.

4. A microorganism harboring a recombinant vector in a third aspect of the invention and expressing the gene.

5. A microorganism in a fourth aspect of the invention, wherein the microorganism is a fungus producing the substance PF1022.

6. A method for producing the substance PF1022 and a derivative thereof by using a microorganism in a fourth or fifth aspect of the invention.

[0010]

#### Mode for Carrying out the Invention

The cyclic depsipeptide synthetase gene of the invention can be isolated from a fungus producing the substance PF1022 for example by the following method.

[0011]

A library comprising the genomic DNA of a fungus producing the substance PF1022 is prepared by extracting the genomic DNA from the fungus producing the substance PF1022, cleaving the DNA with an appropriate restriction endonuclease, and subsequently ligating to a phage vector.

Based on the conserved region of the amino acid sequence of a known peptide synthetase and a partial amino acid sequence of the cyclic peptide synthetase purified from the fungus producing the substance PF1022, an appropriate primer is synthesized, which is used to effect polymerase chain reaction (PCR) with the genomic DNA derived from the fungus producing the substance PF1022 as template, to amplify a DNA fragment of the cyclic peptide synthetase gene. Using the DNA fragment as probe, the genome library is screened. In such manner, the whole region of the cyclic peptide synthetase gene can be

isolated. After the determination of the nucleotide sequence of the DNA fragment, appropriate restriction cleavage sites are introduced upstream the translation initiation codon and downstream the translation termination codon by means such as PCR, to recover a gene fragment singly containing the cyclic peptide synthetase gene.

[0012]

The gene of the invention encompasses a nucleotide sequence hybridizable with the thus determined nucleotide sequence under stringent conditions. Using routine methods (for example site-directed mutagenesis) in the field of genetic engineering, additionally, DNA fragments with modification of the gene, such as addition, insertion, deletion or substitution of the gene, can be encompassed within the scope of the invention. The stringent conditions herein referred to mean that the rinsing procedure of the membrane after hybridization is carried out in solutions at low salt concentrations and high temperature, for example, a condition such that rinsing is effected in  $0.2 \times \text{SSC}$  ( $1 \times \text{SSC}$ : 15 mM citrate trisodium, 150 mM sodium chloride) - 0.1 % SDS solution at  $60^\circ\text{C}$  for 15 minutes.

[0013]

A promoter is conjugated upstream the cyclic peptide synthetase gene isolated by the method, while a terminator is conjugated downstream the cyclic peptide synthetase gene; additionally, selective marker genes such as nutrient auxotrophic complementary genes or/and genes with chemical resistance are conjugated thereto, to prepare a recombinant vector for gene expression.

[0014]

The selective markers for use in recombinant vectors for

gene expression include for example nutrient auxotrophic complementary genes such as pyrG, argB, trpC, niaD, TRP1, LEU2 and URA3; and genes with chemical resistance against destomycin, benomil, oligomycin, hygromycin, G418, bleomycin, fleomycin, phosphinothricin, ampicillin, and kanamycin.

[0015]

The conjugation of the promoter and terminator to the inventive gene and the insertion thereof into a vector can be carried out by methods known per se. The promoter and terminator for use in accordance with the invention are not specifically limited, and include for example, genes of glycolytic enzymes, such as 3-phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase and enolase; genes of amino acid synthesis, such as ornithine carbamoyltransferase and tryptophan synthase; genes of hydrolases, such as amylase, protease, lipase, cellulase and acetoamidase; genes of oxidoreductases, such as nitrate reductase, orotidine-5'-phosphate dehydrogenase, and alcohol dehydrogenase; and genes of bacteria producing the substance PF1022, which are highly expressed in the fungus producing the substance PF1022, such as Abp1.

[0016]

The transformation of a host with a recombinant vector prepared in such manner and the culturing of the resulting transformant enable prominent production of the substance PF1022. For a host with no synthesis of L-leucine, D-lactic acid or D-phenyllactic acid as a substrate for the cyclic depsipeptide synthetase of the invention, additionally, the host is cultured after addition of deficient substrates or derivatives thereof, whereby the substance PF1022 or

derivatives thereof can be produced. The invention also encompasses the culturing of the transformant in a culture medium to collect the substance PF1022 or a derivative thereof from the resulting microorganisms.

[0017]

As the host for use, appropriate bacteria or fungal microorganisms usable as hosts for gene recombination can be used, with no specific limitation. Preferably, the host is Escherichia coli, a bacterium of the genus Bacillus, an actinomycetes, yeast and a filamentous fungus; more preferably, the host is a filamentous fungus producing the substance PF1022; and most preferably, the host is the strain PF1022 (Mycelia sterilia, FERM BP-2671).

[0018]

The transformation of such host can be carried out by methods known per se. For example, the introduction of a recombinant vector for gene expression into a host can be carried out by routine methods, for example electroporation process, polyethylene glycol process, Agrobacterium process, lithium process, calcium chloride process and the like, with no specific limitation.

[0019]

The transformant can also be cultured by general methods, by appropriately selecting culture media and culturing conditions and the like. As the culture media, use can be made of routine components, such as carbon sources for example glucose, sucrose, thick malt syrup, dextrin, starch, glycerol, molasses, animal and vegetable oils and the like. As the nitrogen source, additionally, use can be made of soy bean powder, wheat germ, pharmamedia, corn steep liquor, cotton seed

bran, meat extract, polypeptone, malt extract, yeast extract, ammonium sulfate, sodium nitrate, urea and the like. Additionally, it is effective to add inorganic salts capable of generating sodium, potassium, calcium (calcium carbonate and the like), magnesium, cobalt, chloride, phosphorus (dipotassium hydrogen phosphate), sulfuric acid (magnesium sulfate and the like) and other ions, if necessary. If necessary, furthermore, selective chemical agents including various vitamins such as thiamine (thiamine chloride salt and the like), amino acids such as glutamic acid (sodium glutamate and the like) and asparagine (DL-asparagine and the like), trace nutrients such as nucleotide and antibiotics can be added. Organic materials and inorganic materials supporting fungal growth and promoting the production of the substance PF1022 or a derivative thereof can appropriately be added.

[0020]

The pH of the culture medium is about pH 6 to pH 8. As the culturing method, agitation culture, aerated agitation culture or submerged aerobic culture under aerobic conditions can be carried out. Particularly, submerged aerated culture is the most appropriate. The temperature appropriate for culturing is 15°C to 40°C. In many cases, the microorganism grows around 26°C to 37°C. The production of the substance PF1022 or a derivative thereof varies, depending on the culture medium and culture conditions or the host used, but the accumulation thereof generally reaches the peak in 2 days to 25 days by any of the culture methods. Just when the amount of the substance PF1022 or a derivative thereof reaches the peak, the culturing is terminated, to isolate and purify the objective substance from the culture.

[0021]

So as to recover the substance PF1022 or a derivative thereof from the culture, general separation means utilizing the characteristic properties, for example solvent extraction method, ion exchange resin method, adsorption or partition column chromatography method, gel filtration method, dialysis method, precipitation method and crystallization method, can be used singly or in appropriate combinations thereof to extract and purify the substance PF1022 or a derivative thereof. From the culture, for example, the substance PF1022 or a derivative thereof is extracted in acetone, methanol, butanol, ethyl acetate, butyl acetate and the like. So as to further purify the substance PF1022 or a derivative thereof, chromatography using Sephadex LH-20 (Pharmacia Co.) or Toyopearl HW-40 (Toso, Co.) is satisfactorily effected. By the methods described above or combinations thereof, the substance PF1022 or a derivative thereof can be recovered in purity.

[0022]

#### Examples

The present invention will now be described in the following examples, but the invention is not limited to them.

[0023]

#### Example 1

Cloning of cyclic depsipeptide synthetase gene from a fungus producing the substance PF1022

##### 1. Genomic DNA isolation and preparation of genome library

With UV irradiation or NTG treatment, mutation was induced into the fungus (Mycelia sterilia; FERM BP-2671) producing the substance PF1022, to prepare a fungal strain 432-26 producing the substance PF1022 and having an improved

productivity of PF1022, from which the genome DNA was extracted. The fungal strain 432-26 producing the substance PF1022 was cultured in 50-ml of a seed culture medium [1 % yeast extract, 1 % malt extract, 2 % polypeptone, 2.5 % glucose, 0.1 % dipotassium hydrogen phosphate, 0.05 % magnesium sulfate (pH 7.0)] at 26°C for 2 days, to recover the fungi by centrifugation. The resulting fungi were frozen in liquid nitrogen and ground in a mortar with a pestle. From the ground fungi, the genome DNA was isolated by ISOPLANT (Nippon Gene, Co.) according to the attached protocol. The isolated genome DNA was partially digested with Sau3A I, to recover DNA fragments of 15 kb to 20 kb by agarose gel electrophoresis, which were then treated with alkali phosphatase to dephosphorylate the termini of the DNA fragments. The DNA fragments were inserted in a phage vector Lambda DASH II (STRATAGENE, CO.). The recombinant phage vector recovered in such manner was subjected to in vitro packaging with Gigapack III Gold Packaging Extract (STRATAGENE CO.) according to the attached protocol. Subsequently, the recombinant phage grew on the host Escherichia coli strain XL1-Blue MRA (P2) for plaque formation on a plate.

[0024]

## 2. Isolation of partial DNA fragment of cyclic depsipeptide synthetase gene

A known peptide synthetase was subjected to multiple alignment, so that WTSMYDG and VVQYFPT were detected as excellently conserved regions. Based on these sequences, primers 5'-TGGACIWSNATGTAYGAYGG-3' (SQ ID NO. 3) and 5'-GTIGGRAARTAYTGIACNAC-3' (SQ ID NO. 4) were synthesized. Using these primers, the genome DNA isolated from the fungus producing the substance PF1022 was used as template for PCR. Using 50

ng of the genome DNA as template, 1.25 units ExTaq DNA polymerase (TaKaRa Brewery, Co.), the attached buffer and dNTP mixture, and 10  $\mu$ M primer in 50  $\mu$ l of a reaction solution, PCR was conducted under the following conditions: 94°C for 3 minutes [94°C for one minute, 65°C (with 0.5°C decrement per one cycle) for one minute, 72°C for one minute]  $\times$  30 times and 72°C for 3 minutes. Through the reaction, a DNA fragment of about 350 bp was amplified; and the resulting DNA fragment was inserted in pCR2.1 plasmid vector, by using Original TA Cloning Kit (Invitrogen Co.) according to the attached protocol.

[0025]

The nucleotide sequence of the thus cloned DNA fragment was determined, by using DNA sequencing Kit dRhodamine Terminator Cycle Sequencing Ready Reaction (Perkin Elmer Co.) and ABI PRISM 310 Genetic Analyzer (Perkin Elmer Co.) according to the attached protocol. Consequently, the nucleotide sequence of the isolated DNA fragment was homologous to the peptide synthetase gene, which apparently indicates that the DNA fragment was a part of the objective cyclic depsipeptide synthetase gene.

[0026]

### 3. Cloning of the whole region of the cyclic depsipeptide synthetase gene

The probe for use in the screening of the genome library was prepared, by PCR to allow the DNA fragment to incorporate fluorescein-labeled dUTP. By using pCR2.1 plasmid vector inserted with 100 ng of the DNA fragment of the cyclic depsipeptide synthetase gene as template, 1.25 units ExTaq DNA polymerase (TaKaRa Brewery, Co.) and the attached buffer, 0.2 mM dATP, 0.2 mM dCTP, 0.2 mM dGTP, 0.02 mM dTTP, 0.18 mM

fluorescein-labeled dUTP (FluoroGreen; Amersham Co.) and 10  $\mu$ M primers (SQ ID Nos. 3 and 4) in 50  $\mu$ l of a reaction solution, PCR was carried out under the following conditions: 94°C for 2 minutes, (94°C for 30 seconds, 55°C for one minute and 72°C for one minute)  $\times$  25 times, 72°C for 3 minutes. Through the reaction, a fluorescein-labeled probe of about 350 bp was prepared.

[0027]

On the plate with formed plaques as prepared in Example 1.1, Hybond-N+ membrane (Amersham Co.) was mounted, to deposit the plaques. The membrane was treated with an alkali, to denature the recombinant phage DNA on the membrane into a single strand and thereby adsorb the DNA on the membrane. The phage DNA-adsorbed membrane was placed in a buffer prepared by using Hybridization Buffer Tablets (Amersham Co.), for incubation at 60°C for one hour. The fluorescein-labeled probe was denatured and added to the resulting incubation mixture, for overnight hybridization at 60°C. Thereafter, the membrane was rinsed in 1  $\times$  SSC (SSC: 15 mM citrate trisodium, 150 mM sodium chloride)-0.1 % SDS solution at 60°C for 15 minutes and further rinsed in 0.2  $\times$  SSC-0.1 % SDS solution at 60°C for 15 minutes. The fluorescein-bound plaque was visualized by using DIG-wash and block buffer set (Boehringer Mannheim, Co.), alkali phosphatase-labeled anti-fluorescein antibody (Anti-fluorescein-AP, Fab fragment, Boehringer Mannheim Co.), a chromogenic substrate nitroblue tetrazolium chloride (Boehringer Mannheim Co.) and X-phosphate (Boehringer Mannheim Co.) according to the attached protocol. In such manner, a positive clone carrying the 5' upstream region and 3' downstream region of a region homologous to the probe was screened.

[0028]

4. Determination of the nucleotide sequence

The DNA fragment in the positive clone thus isolated was amplified by PCR using primers 5'-GCGGAATTAACCCCTCACTAAAGGGAACGAA -3' (SQ ID No. 5) and 5'-GCGTAATACGACTCACTATAGGGCGAAGAA-3' (SQ ID No. 6) as the phage vector sequences. Using 100 ng of the positive clone DNA as template, 2.5 units LA Taq DNA polymerase (TaKaRa Brewery, Co.), the attached buffer and dNTP mixture, 2.5 mM magnesium chloride, and 0.2  $\mu$ M primer in a reaction solution of 50  $\mu$ l, PCR was effected under the following conditions: 94°C for one minute, (98°C for 10 seconds and 68°C for 15 minutes)  $\times$  25 times, 72°C for 15 minutes. The resulting PCR product was purified and treated with a nebulizer, to be decomposed randomly into fragments of 0.5 kb to 2.0 kb. The termini of the resulting fragments were blunt ended with T4 DNA polymerase and phosphorylated with T4 polynucleotide kinase, to be then inserted at the EcoRV site of pT7Blue (Novagen Co.) for insertion in Escherichia coli strain JM109. 168 colonies thus prepared were directly subjected to PCR using M13 Primer M4 (TaKaRa Brewery, Co.) and M13 primer RV (TaKaRa Brewery, Co.) and were then purified, which were then sequenced by using M13 primer M4 (TaKaRa Brewery, Co.). Using 1.25 units ExTaq DNA polymerase (TaKaRa Brewery, Co.), the attached buffer and dNTP mixture, and 0.5  $\mu$ M primer, PCR was effected in 50  $\mu$ l of a reaction solution under the following conditions: 94°C for 4 minutes, (94°C for 30 seconds, 55°C for 30 seconds and 72°C for 2 minutes)  $\times$  30 times, 72°C for 3 minutes. Additionally, sequencing was effected, by using DNA Sequencing Kit dRhodamine Terminator Cycle Sequencing Ready Reaction (Perkin Elmer Co.)

and ABI PRISM 310 Genetic Analyzer (Perkin Elmer Co.) according to the attached protocol.

[0029]

Based on the results, an insufficiently analyzed region was amplified by PCR using a primer newly designed on the basis of the analyzed nucleotide sequence and was then purified. Using the primer used for PCR, the region was sequenced, whereby the 15606-bp nucleotide sequence of the DNA fragment in the positive clone was determined.

[0030]

The analysis of the sequence apparently indicates that an open reading frame (ORF) of 9633 bp was present and a protein speculated from the sequence comprised 3210 amino acid residues of 353 kDa and that the protein was homologous to the peptide synthetase. Additionally, the protein with the highest homology was enniatin synthetase (S39842) with 56 % homology. The nucleotide sequence and amino acid sequence of the ORF of the cyclic depsipeptide synthetase gene thus isolated in accordance with the invention are shown as SQ ID Nos. 1 and 2, respectively in the sequence listing.

[0031]

Example 2

Improvement of PF1022 productivity due to the excess expression of cyclic depsipeptide synthetase gene

1. Construction of recombinant vector for gene expression (Fig. 1)

From the positive clone recovered in Example 1.3, plasmid pPF7 was prepared by cleaving the inserted DNA fragment with NotI and inserting the DNA fragment into the NotI site of the pBluescriptII KS+ (STRATAGENE CO.). pPF7 was cleaved with

BanIII and SmaI and elecrophoresed on agarose gel, to recover a DNA fragment of about 8250 bp from the agarose gel. The fragment was inserted in pBluescriptII KS+, to prepare plasmid pPF7-1.

[0032]

Using pPF7 as template, 5'-AGCATCGGATCCTAACAAATGGCGTTGAGCAGCAAGCCCTA-3' (SQ ID No. 7; designed for the initiation of the translation at the 9-th Met from the N terminus of the ORF) or 5'-AGCATCGGATCCTAACAAATGTCAAACATGGCACCCTCCCTA-3' (SQ ID No. 13; designed for the initiation of the translation at the first Met from the N terminus of the ORF), and 5'-TTTGCTTCGTACTCGGGTCCT-3' (SQ ID No. 8) as primers for the amplification of a region of about 440 bp (using SQ ID Nos. 7 and 8) or a region of about 470 bp (using SQ ID Nos. 13 and 8) around the N terminus to the BanIII site, and 5'-GCATCGCGATACTAGAGAAG-3' (SQ ID No. 9) and 5'-AGCATCGAATTGGATCCCTAAACCAACGCCAAAGCCCGAAT-3' (SQ ID No. 10) as primers for the amplification of a region of about 920 bp from the SmaI site to the C terminus, PCR was effected. Then, the primers were designed so as to insert the BamHI site at the 5' and 3' sites of the inventive cyclic depsipeptide synthetase gene. Using 150 ng of the plasmid DNA as template, 2.5 units KOD DNA polymerase (Toyo Boseki), the attached buffer and dNTP mixture, 1 mM magnesium chloride, and 0.5  $\mu$ M primer in 50  $\mu$ l of a reaction solution, PCR was effected under the following conditions: 98°C for 30 seconds, (98°C for 15 seconds, 65°C for 2 seconds, 74°C for 30 seconds)  $\times$  10 times, 74°C for one minute. The PCR reaction solutions recovered by using the individual primers were precipitated with ethanol, to recover PCR products. Concerning the N terminal region, the N terminal region was

cleaved with BamHI and BanIII; concerning the C terminal region, the C terminal region was cleaved with SmaI and BamHI. Thereafter, the resulting fragments were electrophoresed on agarose gel, to recover DNA fragments from the agarose gel.

[0033]

The PCR fragment of the C terminal region was inserted in the SmaI and BamHI sites of pPF7-1, to prepare plasmid pPF7-2. The plasmid was cleaved with BanIII and BamHI and electrophoresed on agarose gel, to recover a DNA fragment of about 9170 bp from the agarose gel. The DNA fragment and the N terminal region prepared by using SQ ID Nos. 7 and 8 were simultaneously inserted in the BamHI site of pBluescript II KS+, to reconstruct the cyclic depsipeptide synthetase gene of the invention and prepare plasmid pPFsyn (initiating the translation at the 9-th Met from the N terminus of the ORF).

[0034]

Alternatively, an about 9170-bp DNA fragment cleaved from pPF7-2 and the N-terminal region prepared by using SQ ID Nos. 7 and 13 were simultaneously inserted in the BamHI site of pHSG299 (TaKaRa Brewery Co.), to reconstruct the cyclic depsipeptide synthetase gene of the invention and prepare plasmid pPFsynN (initiating the translation at the first Met from the N terminus of the ORF). In such manner, the cyclic depsipeptide synthetase gene with the BamHI sites on both the termini was prepared.

[0035]

Herein, Escherichia coli transformed with the plasmid pPFsyn (Escherichia coli DH5 $\alpha$ ) was deposited with Accession No. FERM P-17541 at National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, supra.

[0036]

Additionally, Escherichia coli transformed with the plasmid pPFsynN (Escherichia coli DH5 $\alpha$ ) was deposited with Accession No. FERM P-17542 at National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, *supra*.

[0037]

pPFsyn or pPFsynN was cleaved with BamHI. Subsequently, the cyclic depsipeptide synthetase gene region was recovered from the individual gels. The gene region was inserted at the BamHI site of pABPd with the promoter and terminator of Abp1 gene described in Japanese Patent Application 252851/1999, to prepare an expression vector pABP/PFsyn (initiating the translation at the 9-th Met of the N terminus of ORF) and an expression vector pABP/PFsynN (initiating the translation at the first Met of the N terminus of ORF) as the expression vectors for expressing the cyclic depsipeptide synthetase gene of the invention.

[0038]

2. Introduction and expression of cyclic depsipeptide synthetase gene in fungus producing the substance PF1022

The expression vectors were introduced in a fungus producing the substance PF1022 (Mycelia sterilia; FERM BP-2671) according to the method of Example 1 described in WO 97/00944, to screen strains with high resistance against hygromycin B. The introduction of the objective gene in these strains was confirmed by PCR using a primer 5'- TGATATGCTGGAGCTTCCCT -3' (SQ ID No. 11) prepared from the sequence of Abp1 promoter and a primer 5'- GCACAAACCTTTCCAGGCT -3' (SQ ID No. 12) prepared from the sequence of the cyclic depsipeptide synthetase gene. In

such manner, gene-introduced strains with high resistance against hygromycin B and with the inventive cyclic depsipeptide synthetase gene introduced therein were screened.

[0039]

The gene-introduced strains and the parent strain (Mycelia sterilia; FERM BP-2671) were separately cultured in 50 ml of a seed culture medium at 26°C for 2 days; 1 ml of each of the cultures was inoculated separately in a generation culture medium [6 % thick malt syrup, 2.6 % starch, 2 % wheat germ, 1 % pharmamedia, 0.2 % magnesium sulfate 7 hydrates, 0.2 % calcium carbonate, 0.3 % sodium chloride (pH 7.5)] and cultured therein at 26°C for 4 days. The resulting culture was centrifuged at 4500 rpm for 5 minutes to harvest the fungus; the resulting individual fungus species were rinsed in 0.3 M potassium chloride. The individual fungal species were frozen in liquid nitrogen and freeze-dried.

[0040]

The following extraction procedure was carried out on ice or in a low-temperature chamber at 4°C. Into a 2-ml tube containing 10 mg of the freeze-dried fungal species and 1.0 ml of glass beads (0.5-mm diameter) was added 1.0 ml of an extraction buffer [50 mM Tris-HCl (pH 8.0), 0.3 M potassium chloride, 60 % glycerol, 10 mM ethylenediaminetetraacetate disodium, 5 mM dithiothreitol, 10 µM leupeptin, 1 mM phenylmethanesulfonic acid, 60 µg/ml chymostatin]. The microtube was set in a Mini-Bead-Beater-8 (Biospec, Co.), which was then driven at the maximum speed for 3 minutes for extraction. The resulting mixture was centrifuged at 15000 rpm for 5 minutes; 100 µl of the supernatant was charged in and mixed with 100 µl of 10 % trichloroacetic acid solution. After the

solution was left to stand for 15 minutes, the solution was centrifuged at 15000 rpm for 10 minutes. The resulting precipitate was dissolved in 15  $\mu$ l of an alkali solution (2 % sodium carbonate, 0.4 % sodium hydroxide), to which was added 60  $\mu$ l of a sample buffer [125 mM Tris-HCl (pH 6.8), 20 % glycerol, 4 % sodium dodecylsulfate, 10 % 2-mercaptoethanol, 50 mg/l bromophenol blue]. This was heated in boiling water for 5 minutes, and was then electrophoresed [Sodium Dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)] on 4 % to 20 % polyacrylamide gel with an electrophoresis system (Tefco Co.). The polyacrylamide gel after electrophoresis was stained by using Quick-CBB (Wako Pure Chemical Co.) according to the attached protocol. The electrophoresis result of the proteins extracted from the parent strain and the gene-introduced strain with pABP/PFsyn is shown in Fig. 2. Additionally, the electrophoresis result of the proteins extracted from the parent strain and the gene-introduced strain with pABP/PFsynN is shown in Fig. 3.

[0041]

As described above, the expression level of the cyclic depsipeptide synthetase in the gene-introduced strains was distinctively higher than the level in the parent strain.

[0042]

### 3. Extraction and assay of the substance PF1022

The gene-introduced strains and the parent strain were separately cultured in 50 ml of a seed culture medium at 26°C for 2 days; and 1 ml of each of 50 ml of the cultures was inoculated separately in a generation culture medium and cultured therein at 26°C for 6 days. 10 ml each of the cultures was placed and centrifuged at 3000 rpm for 10 minutes; and the

resulting strain were harvested separately. 10 ml of methanol was added to the individual strains, which were vigorously shaken and left to stand for 30 minutes. Thereafter, those were again shaken and centrifuged at 3000 rpm for 10 minutes; the substance PF1022 extracted from the individual strains in the supernatant was assayed by liquid chromatography. As the column, LiChrospher 100 RP-18 (e) (Kanto Chemical CO.) was used; the column temperature was 40°C; the mobile phase was 80 % acetonitrile at a flow rate of 1.0 ml/min; the substance PF1022 was detected on the basis of the absorbance at 210 nm. The retention time of the substance PF1022 under the conditions was 5 minutes to 6 minutes. The experiments were carried out in duplicate. The average values of the assay results of the substance PF1022 extracted from the parent strain and the gene-introduced strain with the pABP/PFsyn are shown in Table 1.

[0043]

Table 1

	Substance PF1022 (μg/ml)
Parent strain	88
Gene-introduced strain	222

[0044]

The substance PF1022 productivity of the gene-introduced strain was about 2.5-fold that of the parent strain. It is apparently shown that the excess expression of the inventive cyclic depsipeptide synthetase elevates the productivity of the substance PF1022.

[0045]

Additionally, the average values of the assay results of the substance PF1022 extracted from the parent strain and the gene-introduced strain with the pABP/PFsynN are shown in Table

2.

[0046]

Table 2

	Substance PF1022 (μg/ml)
Parent strain	29
Gene-introduced strain 1	123
Gene-introduced strain 2	136
Gene-introduced strain 3	172

[0047]

The substance PF1022 productivity of the gene-introduced strains was 4.3- to 6.0-fold that of the parent strain. It is apparently shown that the excess expression of the inventive cyclic depsipeptide synthetase elevates the productivity of the substance PF1022.

[0048]

#### Advantages of the Invention

The introduction of the inventive cyclic depsipeptide synthetase gene in the fungus producing the substance PF1022 can improve the productivity of the substance PF1022.

[0049]

SEQUENCE LISTING

<110> Meiji Seika Kaisha, Ltd

<120> Cyclodepsipeptide synthetase gene

<130> PM1577

<150> JP11-253040

<151> 1999-09-07

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 9633

<212> DNA

<213> Mycelia sterilia

<220>

<221> CDS

<222> (1)..(9633)

<223> peptide synthetase for PF1022

<220>

<221> mat#peptide

<222> (13)..(9630)

<400> 1

atg tca aac atg gca cca ctc cct acg atg ggc gtt gag cag caa gcc 48  
Met Ser Asn Met Ala Pro Leu Pro Thr Met Gly Val Glu Gln Gln Ala  
-1 1 5 10

cta tca ctt tca tgc ccc tta ctc cct cat gac gat gag aaa cac tca 96  
Leu Ser Leu Ser Cys Pro Leu Leu Pro His Asp Asp Glu Lys His Ser  
15 20 25

gac aac ctt tac gag caa gca act cgg cac ttc ggc ttg agc cga gac 144  
Asp Asn Leu Tyr Glu Gln Ala Thr Arg His Phe Gly Leu Ser Arg Asp  
30 35 40

aag atc gaa aat gtc tta cca tgt act tcc ttt caa tgt gat gtc ata 192  
Lys Ile Glu Asn Val Leu Pro Cys Thr Ser Phe Gln Cys Asp Val Ile  
45 50 55 60

gat tgc gcc gtc gac gat cgg cgg cat gct atc ggt cac gtc gtc tat 240  
Asp Cys Ala Val Asp Asp Arg Arg His Ala Ile Gly His Val Val Tyr  
65 70 75

gat atc ccc aat aca gtg gac atc cag cgt tta gcc gca gcc tgg aaa 288  
Asp Ile Pro Asn Thr Val Asp Ile Gln Arg Leu Ala Ala Ala Trp Lys  
80 85 90

gag gtt gtg cgg cag aca cca atc ttg agg acc ggc atc ttt aca tca 336  
Glu Val Val Arg Gln Thr Pro Ile Leu Arg Thr Gly Ile Phe Thr Ser  
95 100 105

gaa acc ggc gac tct ttt cag atc gtc ttg aaa gaa ggc tgc cta ccg 384  
Glu Thr Gly Asp Ser Phe Gln Ile Val Leu Lys Glu Gly Cys Leu Pro

110 115 120

tgg atg tac gcg aca tgt ctc ggc atg aag ggg gca gtg ata caa gat 432  
Trp Met Tyr Ala Thr Cys Leu Gly Met Lys Gly Ala Val Ile Gln Asp  
125 130 135 140

gaa gca gtc gcc gct atg act gga ccg cgt tgc aat cga tat gtc gtc 480  
Glu Ala Val Ala Ala Met Thr Gly Pro Arg Cys Asn Arg Tyr Val Val  
145 150 155

ctg gag gac ccg agt acg aag caa agg ctg ctc atc tgg aca ttc agc 528  
Leu Glu Asp Pro Ser Thr Lys Gln Arg Leu Leu Ile Trp Thr Phe Ser  
160 165 170

cat gct tta gtg gat tat aca gtc cag gaa cgc atc ctt cag cgg gtt 576  
His Ala Leu Val Asp Tyr Thr Val Gln Glu Arg Ile Leu Gln Arg Val  
175 180 185

ctc aca gta tac gac ggc cgg gac gtc gag tgc cct cgc atc aag gat 624  
Leu Thr Val Tyr Asp Gly Arg Asp Val Glu Cys Pro Arg Ile Lys Asp  
190 195 200

aca gaa cat gtc tct cgg ttt tgg caa caa cac ttt gaa ggc tta gat 672  
Thr Glu His Val Ser Arg Phe Trp Gln Gln His Phe Glu Gly Leu Asp  
205 210 215 220

gcc tcc gta ttt ccc ctt cta cca tct cac cta act gtg tgc aat ccc 720  
Ala Ser Val Phe Pro Leu Leu Pro Ser His Leu Thr Val Cys Asn Pro  
225 230 235

aat gcg cgc gca gaa cat cat atc tca tac acg gga cca gtc cag agg 768  
Asn Ala Arg Ala Glu His His Ile Ser Tyr Thr Gly Pro Val Gln Arg  
240 245 250

aag tgg tcc cat aca agt atc tgt cgg gct gca ctc gca gtt ctt cta 816  
Lys Trp Ser His Thr Ser Ile Cys Arg Ala Ala Leu Ala Val Leu Leu  
255 260 265

tct cgc ttt aca cac tct tcg gag gcc ctc ttc ggt gtt gtg aca gaa 864  
Ser Arg Phe Thr His Ser Ser Glu Ala Leu Phe Gly Val Val Thr Glu  
270 275 280

caa tct cac aac tcc gag gac caa aga cgg tca att gat ggc ccc gca 912  
Gln Ser His Asn Ser Glu Asp Gln Arg Arg Ser Ile Asp Gly Pro Ala  
285 290 295 300

agg aca gta gtg cct atc cgc gtc ctt tgt gcc cca gat caa tat gtg 960  
Arg Thr Val Val Pro Ile Arg Val Leu Cys Ala Pro Asp Gln Tyr Val  
305 310 315

tcg gat gtc att ggg gca atc acc gca cac gaa cac gcc atg cgc ggg 1008  
Ser Asp Val Ile Gly Ala Ile Thr Ala His Glu His Ala Met Arg Gly  
320 325 330

ttt gag cac gct gga ctt cgc aat atc cgc cgt acc gga gac gac ggg 1056

Phe Glu His Ala Gly Leu Arg Asn Ile Arg Arg Thr Gly Asp Asp Gly

335

340

345

tct gct gct tgt gga ttc cag acc gtg cta ctg gtg act gac ggt gat 1104

Ser Ala Ala Cys Gly Phe Gln Thr Val Leu Leu Val Thr Asp Gly Asp

350

355

360

gct ccc aag acc cct ggg agt gta ctt cat cga agt gta gaa gaa tcg 1152

Ala Pro Lys Thr Pro Gly Ser Val Leu His Arg Ser Val Glu Glu Ser

365

370

375

380

gat aga ttc atg ccc tgc gct aat cgt gcc ctt ctg ctc gac tgc cag 1200

Asp Arg Phe Met Pro Cys Ala Asn Arg Ala Leu Leu Asp Cys Gln

385

390

395

atg gct ggc aac tcg gca tcc cta gtc gca cga tat gat cat aat gtg 1248

Met Ala Gly Asn Ser Ala Ser Leu Val Ala Arg Tyr Asp His Asn Val

400

405

410

atc gac cca cgc cag atg tct cgc ttc ctg cga cag cta gga tac ctg 1296

Ile Asp Pro Arg Gln Met Ser Arg Phe Leu Arg Gln Leu Gly Tyr Leu

415

420

425

atc caa caa ttt cat cat cac gtc gat ctg cct ctg gtc aaa gaa ctg 1344

Ile Gln Gln Phe His His Val Asp Leu Pro Leu Val Lys Glu Leu

430

435

440

gac gtc gtg acg gcg gag gat tgt gcg gaa atc gag aaa tgg aat tca 1392

Asp Val Val Thr Ala Glu Asp Cys Ala Glu Ile Glu Lys Trp Asn Ser

445 450 455 460

gaa cgc cta aca atg caa gac gcc tta atc cac gac acc ata tcc aag 1440  
Glu Arg Leu Thr Met Gln Asp Ala Leu Ile His Asp Thr Ile Ser Lys

465 470 475

tgg gct gct ggc gat ccc aac aaa gct gca gtt ttc gct tgg gat ggg 1488  
Trp Ala Ala Gly Asp Pro Asn Lys Ala Ala Val Phe Ala Trp Asp Gly  
480 485 490

gaa tgg aca tac gcc gag cta gac aac ata tcc tcc cgt ctc gcc gtg 1536  
Glu Trp Thr Tyr Ala Glu Leu Asp Asn Ile Ser Ser Arg Leu Ala Val  
495 500 505

tat atc caa tcc ctg gac ttg aga cca gga caa gca ata ctc cca ctc 1584  
Tyr Ile Gln Ser Leu Asp Leu Arg Pro Gly Gln Ala Ile Leu Pro Leu  
510 515 520

tgc ttc gag aag tca aaa tgg gtc gtc gcc aca att ctc gcc gtc ctc 1632  
Cys Phe Glu Lys Ser Lys Trp Val Val Ala Thr Ile Leu Ala Val Leu  
525 530 535 540

aaa gtc ggt cgg gca ttc aca ctc atc gac ccg tgc gac ccc tcg gca 1680  
Lys Val Gly Arg Ala Phe Thr Leu Ile Asp Pro Cys Asp Pro Ser Ala  
545 550 555

agg atg gcc cag gtc tgt cag cag acc tcc gcc aca gtc gct ctc acc 1728  
Arg Met Ala Gln Val Cys Gln Gln Thr Ser Ala Thr Val Ala Leu Thr  
560 565 570

tcc aaa ctc cac aac acc acc tta cgt tcc gtc gtt tcc cgc tgc att 1776

Ser Lys Leu His Asn Thr Thr Leu Arg Ser Val Val Ser Arg Cys Ile

575

580

585

gtg gtc gac gac ctc ctt cgg tcc tta ccc cac gcc gat ggc cgc 1824

Val Val Asp Asp Asp Leu Leu Arg Ser Leu Pro His Ala Asp Gly Arg

590

595

600

tta aag gcc acc gtg aag cca cag gac ttg gcc tat gtt att ttc aca 1872

Leu Lys Ala Thr Val Lys Pro Gln Asp Leu Ala Tyr Val Ile Phe Thr

605

610

615

620

tct ggc agc aca gga gag ccg aaa ggc atc atg atc gaa cat cgg ggg 1920

Ser Gly Ser Thr Gly Glu Pro Lys Gly Ile Met Ile Glu His Arg Gly

625

630

635

ttc gtg tcg tgt gct atg aaa ttt ggc ccc gcg ctc gga atg gat gag 1968

Phe Val Ser Cys Ala Met Lys Phe Gly Pro Ala Leu Gly Met Asp Glu

640

645

650

cac acg cgc gct ctt caa ttc gcc tca tat gcg ttt ggc gct tgt ctg 2016

His Thr Arg Ala Leu Gln Phe Ala Ser Tyr Ala Phe Gly Ala Cys Leu

655

660

665

gta gaa gtt gtg aca gct ctg atg cac ggc ggc tgc gtc atc cct 2064

Val Glu Val Val Thr Ala Leu Met His Gly Gly Cys Val Cys Ile Pro

670

675

680

tcc	gat	gac	gat	cgc	ttg	aac	aat	gta	ccg	gag	ttc	atc	aaa	agg	gcc	2112
Ser	Asp	Asp	Asp	Arg	Leu	Asn	Asn	Val	Pro	Glu	Phe	Ile	Lys	Arg	Ala	
685															700	
cag	gtg	aac	tgg	gtg	ata	ctc	act	ccg	tcg	tat	atc	ggg	aca	ttc	cag	2160
Gln	Val	Asn	Trp	Val	Ile	Leu	Thr	Pro	Ser	Tyr	Ile	Gly	Thr	Phe	Gln	
															715	
705								710								
ccg	gaa	gat	gtc	cct	gga	cta	caa	aca	ctg	gta	ttg	gtt	gga	gaa	cct	2208
Pro	Glu	Asp	Val	Pro	Gly	Leu	Gln	Thr	Leu	Val	Leu	Val	Gly	Glu	Pro	
720								725							730	
atc	tca	gcg	tct	att	cg	gat	acc	tgg	gcc	tcc	cag	gtt	cga	ctc	ctg	2256
Ile	Ser	Ala	Ser	Ile	Arg	Asp	Thr	Trp	Ala	Ser	Gln	Val	Arg	Leu	Leu	
735								740							745	
aat	gcc	tac	ggt	cag	agt	gaa	agc	tca	act	atg	tgc	agc	gtc	acg	gaa	2304
Asn	Ala	Tyr	Gly	Gln	Ser	Glu	Ser	Ser	Thr	Met	Cys	Ser	Val	Thr	Glu	
750								755							760	
gtc	agc	ccg	ctc	tcc	ctc	gaa	ccg	aac	aat	atc	ggt	cg	gct	gta	ggc	2352
Val	Ser	Pro	Leu	Ser	Leu	Glu	Pro	Asn	Asn	Ile	Gly	Arg	Ala	Val	Gly	
765								770							775	
780																
gca	cga	tcc	tgg	atc	att	gat	ccc	gac	gag	cct	gat	cgt	ctt	gct	cca	2400
Ala	Arg	Ser	Trp	Ile	Ile	Asp	Pro	Asp	Glu	Pro	Asp	Arg	Leu	Ala	Pro	
785								790							795	
att	ggc	tgc	att	gga	gag	cta	gtg	atc	gaa	agt	ccg	ggc	att	gcg	cgc	2448

Ile Gly Cys Ile Gly Glu Leu Val Ile Glu Ser Pro Gly Ile Ala Arg

800

805

810

gac tat atc atc gcg ccg ccg gac aag tcc ccc ttt ctc cta gca 2496

Asp Tyr Ile Ile Ala Pro Pro Pro Asp Lys Ser Pro Phe Leu Leu Ala

815

820

825

ccc ccg gcc tgg tat cca gcc ggg aaa tta tcc aac gcc ttt aaa ttt 2544

Pro Pro Ala Trp Tyr Pro Ala Gly Lys Leu Ser Asn Ala Phe Lys Phe

830

835

840

tac aag act gga gat ctc gtg cgt tat gga cct gac ggc acc atc gtc 2592

Tyr Lys Thr Gly Asp Leu Val Arg Tyr Gly Pro Asp Gly Thr Ile Val

845

850

855

860

tgc ctg gga cgc aaa gat tcg caa gtg aag atc cga ggg cag cgc gta 2640

Cys Leu Gly Arg Lys Asp Ser Gln Val Lys Ile Arg Gly Gln Arg Val

865

870

875

gag atc agc gca gtg gaa gcc agt cta cga cga caa cta cct agt gac 2688

Glu Ile Ser Ala Val Glu Ala Ser Leu Arg Arg Gln Leu Pro Ser Asp

880

885

890

atc atg ccc gtg gcc gaa gct atc aaa cgc tcg gat tcg tca ggc agc 2736

Ile Met Pro Val Ala Glu Ala Ile Lys Arg Ser Asp Ser Ser Gly Ser

895

900

905

aca gtc ttg act gcc ttc ttg ata ggg tca tct aag agc gga gat ggt 2784

Thr Val Leu Thr Ala Phe Leu Ile Gly Ser Ser Lys Ser Gly Asp Gly

910

915

920

aat ggc cac gct tta tct gcg gca gac gcc gtt atc ttg gat cac ggt 2832  
Asn Gly His Ala Leu Ser Ala Ala Asp Ala Val Ile Leu Asp His Gly

925 930 935 940

gct acc aac gag ata aac gcg aag ttg cag caa atc ctt ccc cag cat 2880  
Ala Thr Asn Glu Ile Asn Ala Lys Leu Gln Gln Ile Leu Pro Gln His

945 950 955

tcc gtt cca tcc tat tat atc cac atg gaa aat ctt cct cga act gcc 2928  
Ser Val Pro Ser Tyr Tyr Ile His Met Glu Asn Leu Pro Arg Thr Ala

960 965 970

acc ggc aaa gcg gac agg aaa atg ctt cga tct att gct agc aag cta 2976  
Thr Gly Lys Ala Asp Arg Lys Met Leu Arg Ser Ile Ala Ser Lys Leu

975 980 985

ttg ggt gaa ttg tct cag aac gtg aca tct caa ccg att gag aag cac 3024  
Leu Gly Glu Leu Ser Gln Asn Val Thr Ser Gln Pro Ile Glu Lys His

990 995 1000

gat gcc cca gca act ggt ata gag gtc aag ctg aag gag ctt tgg ttt 3072  
Asp Ala Pro Ala Thr Gly Ile Glu Val Lys Leu Lys Glu Leu Trp Phe

1005 1010 1015 1020

ctg agc ttg aat ctt aat ccc aac tct caa gat gtc gga gcg agt ttc 3120  
Leu Ser Leu Asn Leu Asn Pro Asn Ser Gln Asp Val Gly Ala Ser Phe

1025 1030 1035

ttt gac tta ggc gga aat tcc att atc gcc atc aaa atg gta aac aac atg 3168  
Phe Asp Leu Gly Gly Asn Ser Ile Ile Ala Ile Lys Met Val Asn Met  
1040 1045 1050

gcg agg tca gct ggg ata gca ctg aag gta tcc gac ata ttc cag aat 3216  
Ala Arg Ser Ala Gly Ile Ala Leu Lys Val Ser Asp Ile Phe Gln Asn  
1055 1060 1065

ccc acg ctc gcc ggc ctt gtg gat gtc atc ggg cga gac ccg gct ccg 3264  
Pro Thr Leu Ala Gly Leu Val Asp Val Ile Gly Arg Asp Pro Ala Pro  
1070 1075 1080

tac aac ctc atc cca aca aca gca tac agc gga cct gtt gag cag tcg 3312  
Tyr Asn Leu Ile Pro Thr Thr Ala Tyr Ser Gly Pro Val Glu Gln Ser  
1085 1090 1095 1100

ttc gcc cag ggc cgt cta tgg ttc ttg gac cag atc gaa ctc gat gcg 3360  
Phe Ala Gln Gly Arg Leu Trp Phe Leu Asp Gln Ile Glu Leu Asp Ala  
1105 1110 1115

ttg tgg tac ctt cta cca tac gcc gtt cgc atg cgc ggg cca ttg cat 3408  
Leu Trp Tyr Leu Leu Pro Tyr Ala Val Arg Met Arg Gly Pro Leu His  
1120 1125 1130

att gat gcg ctc act att gcg ttg cta gct ata cag caa cga cat gaa 3456  
Ile Asp Ala Leu Thr Ile Ala Leu Leu Ala Ile Gln Gln Arg His Glu  
1135 1140 1145

acc ttg cgg aca acc ttt gag gag cag gac ggc gta ggc gtt cag gtt 3504  
Thr Leu Arg Thr Thr Phe Glu Glu Gln Asp Gly Val Gly Val Gln Val  
1150 1155 1160

gtc cat gcg agc ccc atc tcc gac ttg agg ata atc gac gta tca ggc 3552  
Val His Ala Ser Pro Ile Ser Asp Leu Arg Ile Ile Asp Val Ser Gly  
1165 1170 1175 1180

gac cga aac agt gac tac ctc cag ttg cta cac caa gag cag acg act 3600  
Asp Arg Asn Ser Asp Tyr Leu Gln Leu Leu His Gln Glu Gln Thr Thr  
1185 1190 1195

cca ttc att cta gca tgt cag gca gga tgg agg gta tca ctg att aga 3648  
Pro Phe Ile Leu Ala Cys Gln Ala Gly Trp Arg Val Ser Leu Ile Arg  
1200 1205 1210

cta gga gaa gat gat cac atc ctc tct atc gta atg cat cac atc atc 3696  
Leu Gly Glu Asp Asp His Ile Leu Ser Ile Val Met His His Ile Ile  
1215 1220 1225

tcc gac ggc tgg tct atc gac att cta cgc cgg gaa cta agc aat ttc 3744  
Ser Asp Gly Trp Ser Ile Asp Ile Leu Arg Arg Glu Leu Ser Asn Phe  
1230 1235 1240

tat tca gcc gct ctc cgg ggc tct gat cct cta tcg gtg gtg agc cca 3792  
Tyr Ser Ala Ala Leu Arg Gly Ser Asp Pro Leu Ser Val Val Ser Pro  
1245 1250 1255 1260

ctc cca ctc cac tac cgc gac ttt tcc gtt tgg caa aag cag gtc gaa 3840

Leu Pro Leu His Tyr Arg Asp Phe Ser Val Trp Gln Lys Gln Val Glu

1265

1270

1275

cag gag acc gaa cat gag cgg caa ctc gaa tac tgg gtc aag cag ctc 3888  
Gln Glu Thr Glu His Glu Arg Gln Leu Glu Tyr Trp Val Lys Gln Leu

1280

1285

1290

gca gac agc tcg gcc gaa ttc cta acc gac ttc ccc cga ccc aac 3936  
Ala Asp Ser Ser Ala Ala Glu Phe Leu Thr Asp Phe Pro Arg Pro Asn

1295

1300

1305

ata ctg tcc ggt gaa gca ggt tcc gtg cca gtg acg atc gaa ggc gaa 3984  
Ile Leu Ser Gly Glu Ala Gly Ser Val Pro Val Thr Ile Glu Gly Glu  
1310 1315 1320

ctg tat gaa agg ctc caa gaa ttc tgt aaa gta gag caa atg acg cct 4032  
Leu Tyr Glu Arg Leu Gln Glu Phe Cys Lys Val Glu Gln Met Thr Pro  
1325 1330 1335 1340

ttc gcc gtg ttg tta ggg gcc ttc cgc gcg acc cat tat cgt ctc acc 4080  
Phe Ala Val Leu Leu Gly Ala Phe Arg Ala Thr His Tyr Arg Leu Thr  
1345 1350 1355

ggc gcc gaa gac tcg atc atc ggc acg ccc atc gcg aac cgc aac cgc 4128  
Gly Ala Glu Asp Ser Ile Ile Gly Thr Pro Ile Ala Asn Arg Asn Arg  
1360 1365 1370

cag gag ctt gaa aac atg atc ggc ttc ttc gtc aac acc caa tgc atg 4176  
Gln Glu Leu Glu Asn Met Ile Gly Phe Phe Val Asn Thr Gln Cys Met

1375	1380	1385	
cga atc acg gtc gac ggc gac gac act ttt gaa agc ctg gtg cga caa 4224			
Arg Ile Thr Val Asp Gly Asp Asp Thr Phe Glu Ser Leu Val Arg Gln			
1390	1395	1400	
gtt cgg acc acg gcg acg gcg gca ttc gag cac caa gac gtc ccc ttt 4272			
Val Arg Thr Thr Ala Thr Ala Ala Phe Glu His Gln Asp Val Pro Phe			
1405	1410	1415	1420
gag cgc gtc gtg acg gca ctc ctt cca cgc tcg aga gac cta tcc cga 4320			
Glu Arg Val Val Thr Ala Leu Leu Pro Arg Ser Arg Asp Leu Ser Arg			
1425	1430	1435	
aac cca cta gca cag ctc acc ttc gct ctt cat tct caa cag gac ctc 4368			
Asn Pro Leu Ala Gln Leu Thr Phe Ala Leu His Ser Gln Gln Asp Leu			
1440	1445	1450	
ggc aag ttc gag ctg gag ggt ctc gta gcg gaa ccc gtc tcg aac aag 4416			
Gly Lys Phe Glu Leu Glu Gly Leu Val Ala Glu Pro Val Ser Asn Lys			
1455	1460	1465	
gta tac acc agg ttc gac gtg gag ttt cac ctg ttc caa gaa gcc gga 4464			
Val Tyr Thr Arg Phe Asp Val Glu Phe His Leu Phe Gln Glu Ala Gly			
1470	1475	1480	
aga cta agc ggt aac gtg gca ttt gcg gca gat cta ttc aag cct gag 4512			
Arg Leu Ser Gly Asn Val Ala Phe Ala Ala Asp Leu Phe Lys Pro Glu			
1485	1490	1495	1500

acc att agc aat gta gtc gcc ata ttt ttc caa atc ctg cga caa ggc	4560		
Thr Ile Ser Asn Val Val Ala Ile Phe Phe Gln Ile Leu Arg Gln Gly			
1505	1510	1515	
att cgc cag cct cg <sup>g</sup> act cca atc gct gtt ctc cc <sup>g</sup> ctt acc gat ggg	4608		
Ile Arg Gln Pro Arg Thr Pro Ile Ala Val Leu Pro Leu Thr Asp Gly			
1520	1525	1530	
tta gcg gac ctt cgt gcc atg ggc ttg ctt gag atc gag aag gca gaa	4656		
Leu Ala Asp Leu Arg Ala Met Gly Leu Leu Glu Ile Glu Lys Ala Glu			
1535	1540	1545	
ta <sup>c</sup> ccg cgg gag tcg agc gtc gtc gac gtc ttc cgc aag cag gtg gcc	4704		
Tyr Pro Arg Glu Ser Ser Val Val Asp Val Phe Arg Lys Gln Val Ala			
1550	1555	1560	
gct cac ccg cac gct ttt gcc gtt gtc gat tcg gca tcg cgc ctc aca	4752		
Ala His Pro His Ala Phe Ala Val Val Asp Ser Ala Ser Arg Leu Thr			
1565	1570	1575	1580
tat gct gat ctc gat cgt caa tcc gat caa ctc gcg acc tgg ctc ggt	4800		
Tyr Ala Asp Leu Asp Arg Gln Ser Asp Gln Leu Ala Thr Trp Leu Gly			
1585	1590	1595	
cg <sup>g</sup> cgc aat atg acg gct gag acg ctg gtc ggg gtg tta gca ccg cgg	4848		
Arg Arg Asn Met Thr Ala Glu Thr Leu Val Gly Val Leu Ala Pro Arg			
1600	1605	1610	

tca tgt caa aca gtt gtt gcc att tta ggt atc ctg aaa gcg aat ctc 4896  
Ser Cys Gln Thr Val Val Ala Ile Leu Gly Ile Leu Lys Ala Asn Leu  
1615 1620 1625

gca tat ctc ccg ctt gat gtg aat tgt cct acc gcc cgc ctg caa aca 4944  
Ala Tyr Leu Pro Leu Asp Val Asn Cys Pro Thr Ala Arg Leu Gln Thr  
1630 1635 1640

atc cta tct aca ttg aat cgg cac aag ttg gtc cta ctc ggc tct aac 4992  
Ile Leu Ser Thr Leu Asn Arg His Lys Leu Val Leu Leu Gly Ser Asn  
1645 1650 1655 1660

gca act act ccg gat gtc cag ata cct gat gta gag ctg gta cga atc 5040  
Ala Thr Thr Pro Asp Val Gln Ile Pro Asp Val Glu Leu Val Arg Ile  
1665 1670 1675

agc gat atc tta gat cgc ccc atc aat ggc cag gca aag cta aat ggt 5088  
Ser Asp Ile Leu Asp Arg Pro Ile Asn Gly Gln Ala Lys Leu Asn Gly  
1680 1685 1690

cat aca aaa tcg aat ggc tac tca aag cca aac ggc tat acg cat ctg 5136  
His Thr Lys Ser Asn Gly Tyr Ser Lys Pro Asn Gly Tyr Thr His Leu  
1695 1700 1705

aaa ggc tat tca aac cta aac ggt tat tca aaa caa aat ggt tat gca 5184  
Lys Gly Tyr Ser Asn Leu Asn Gly Tyr Ser Lys Gln Asn Gly Tyr Ala  
1710 1715 1720

caa ctc aac ggc cat aga gag cgt aac aat tat tta gat cta aat ggg 5232

Gln	Leu	Asn	Gly	His	Arg	Glu	Arg	Asn	Asn	Tyr	Leu	Asp	Leu	Asn	Gly	
1725																1740
cac tca ctg cta aat ggg aat tca gac atc acc aca tca ggg ccc tca															5280	
His Ser Leu Leu Asn Gly Asn Ser Asp Ile Thr Thr Ser Gly Pro Ser																
																1745
1750															1755	
gca aca agc ctt gcc tac gtg atc ttc aca tcc ggc tca acc gga aag															5328	
Ala Thr Ser Leu Ala Tyr Val Ile Phe Thr Ser Gly Ser Thr Gly Lys																
																1760
1765															1770	
ccc aaa gga gtc atg gtc gaa cac cgc agc atc atc cga ctt gca aag															5376	
Pro Lys Gly Val Met Val Glu His Arg Ser Ile Ile Arg Leu Ala Lys																
																1775
1780															1785	
aag aac aga atc ata tcc agg ttc cca tct gta gcc aag gta gct cac															5424	
Lys Asn Arg Ile Ile Ser Arg Phe Pro Ser Val Ala Lys Val Ala His																
																1790
1795															1800	
ctc tca aac atc gcc ttt gac gcc gcc act tgg gaa atg ttc gca gcc															5472	
Leu Ser Asn Ile Ala Phe Asp Ala Ala Thr Trp Glu Met Phe Ala Ala																
																1805
1810															1815	
1820																
ctt cta aac ggc gga acg ctg gtc tgt atc gac tat atg acc acc ctg															5520	
Leu Leu Asn Gly Gly Thr Leu Val Cys Ile Asp Tyr Met Thr Thr Leu																
																1825
1830															1835	
gac agc aaa acg ctc gag gcc gcg ttt gca cga gaa caa atc aac gcc															5568	
Asp Ser Lys Thr Leu Glu Ala Ala Phe Ala Arg Glu Gln Ile Asn Ala																

1840	1845	1850	
gct tta ctc acg ccc gct ttg ttg aag cag tgc cta gcc aac att ccc			5616
Ala Leu Leu Thr Pro Ala Leu Leu Lys Gln Cys Leu Ala Asn Ile Pro			
1855	1860	1865	
act acc cta ggc agg ctg agt gca ctc gtt att gga ggt gat agg ctt			5664
Thr Thr Leu Gly Arg Leu Ser Ala Leu Val Ile Gly Gly Asp Arg Leu			
1870	1875	1880	
gac ggc caa gac gcg atc gca gca cat gcg ctt gtc ggt gct ggc gtg			5712
Asp Gly Gln Asp Ala Ile Ala Ala His Ala Leu Val Gly Ala Gly Val			
1885	1890	1895	1900
tat aat gcg tat ggc ccg acc gaa aac gga gtg atc agt acg att tat			5760
Tyr Asn Ala Tyr Gly Pro Thr Glu Asn Gly Val Ile Ser Thr Ile Tyr			
1905	1910	1915	
aat atc act aaa aac gac tcg ttc atc aac gga gtc ccc atc ggc tgt			5808
Asn Ile Thr Lys Asn Asp Ser Phe Ile Asn Gly Val Pro Ile Gly Cys			
1920	1925	1930	
gca atc agc aat tcc ggc gcc tac atc aca gac cca gac cag cag ctc			5856
Ala Ile Ser Asn Ser Gly Ala Tyr Ile Thr Asp Pro Asp Gln Gln Leu			
1935	1940	1945	
gta cct cct ggc gtc atg ggt gaa ctc gtc gtt acc ggt gac ggg ctc			5904
Val Pro Pro Gly Val Met Gly Glu Leu Val Val Thr Gly Asp Gly Leu			
1950	1955	1960	

gcg cgg ggg tat aca gac cca gca cta gac gcg ggc cgc ttc gtc cag 5952  
Ala Arg Gly Tyr Thr Asp Pro Ala Leu Asp Ala Gly Arg Phe Val Gln  
1965 1970 1975 1980

atc atg atc aat gac aag gcc gtg agg gcg tac cga acg ggt gac cgg 6000  
Ile Met Ile Asn Asp Lys Ala Val Arg Ala Tyr Arg Thr Gly Asp Arg  
1985 1990 1995

gca cga tat cgc gta gga gac ggt cag atc gag ttc ttc gga cgc atg 6048  
Ala Arg Tyr Arg Val Gly Asp Gly Gln Ile Glu Phe Phe Gly Arg Met  
2000 2005 2010

gat cag caa gtc aag atc cga ggt cac cgc att gaa cca gcc gaa gtg 6096  
Asp Gln Gln Val Lys Ile Arg Gly His Arg Ile Glu Pro Ala Glu Val  
2015 2020 2025

gag cgt gct att ctc gac caa gac tcg gcc cgc gac gcc gtc gtt gtc 6144  
Glu Arg Ala Ile Leu Asp Gln Asp Ser Ala Arg Asp Ala Val Val Val  
2030 2035 2040

atc cgg cac caa gaa ggt gaa gaa ccg gag atg gtt ggt ttc gtc gcg 6192  
Ile Arg His Gln Glu Gly Glu Pro Glu Met Val Gly Phe Val Ala  
2045 2050 2055 2060

acc cac ggc gat cac tct gcc gaa caa gag gaa gca gac gac cag gtt 6240  
Thr His Gly Asp His Ser Ala Glu Gln Glu Glu Ala Asp Asp Gln Val  
2065 2070 2075

gaa ggt tgg aaa gac ttc ttc gag agc aat aca tat gcc gac atg gat 6288  
Glu Gly Trp Lys Asp Phe Phe Glu Ser Asn Thr Tyr Ala Asp Met Asp  
2080 2085 2090

acc atc ggc cag tct gct ata ggc aac gac ttt acg ggc tgg acg tcc 6336  
Thr Ile Gly Gln Ser Ala Ile Gly Asn Asp Phe Thr Gly Trp Thr Ser  
2095 2100 2105

atg tac gac ggg agc gag atc aac aag gcc gag atg cag gag tgg ctc 6384  
Met Tyr Asp Gly Ser Glu Ile Asn Lys Ala Glu Met Gln Glu Trp Leu  
2110 2115 2120

gac gac acc atg cgc aca ctc ctc gat ggc caa gcg ccg ggt cac gta 6432  
Asp Asp Thr Met Arg Thr Leu Leu Asp Gly Gln Ala Pro Gly His Val  
2125 2130 2135 2140

ctc gaa ata ggc aca ggc agt ggc atg gta ttg ttt aac tta ggg gcc 6480  
Leu Glu Ile Gly Thr Gly Ser Gly Met Val Leu Phe Asn Leu Gly Ala  
2145 2150 2155

ggg cta caa agc tac gta ggt ctt gaa cca tct aga tct gca gcc acg 6528  
Gly Leu Gln Ser Tyr Val Gly Leu Glu Pro Ser Arg Ser Ala Ala Thr  
2160 2165 2170

ttt gtt acc aaa gcg atc aat tcc acc cca gct ctt gca gga aag gcc 6576  
Phe Val Thr Lys Ala Ile Asn Ser Thr Pro Ala Leu Ala Gly Lys Ala  
2175 2180 2185

gaa gtg cac gtc ggc aca gcg aca gac ata aac cga ctt cgt gga ctt 6624

Glu Val His Val Gly Thr Ala Thr Asp Ile Asn Arg Leu Arg Gly Leu

2190

2195

2200

cgt ccc gat cta gtt gtg ctc aac tcg gta gtc cag tat ttc ccc acg 6672

Arg Pro Asp Leu Val Val Leu Asn Ser Val Val Gln Tyr Phe Pro Thr

2205

2210

2215

2220

ccc gag tac cta cta gag gtc gtg gag agt ctc gtc cg<sup>g</sup> att ccg ggc 6720

Pro Glu Tyr Leu Leu Glu Val Val Glu Ser Leu Val Arg Ile Pro Gly

2225

2230

2235

gtc aag cgc gtg gtc ttc ggc gac ata cga tct cac gcc acg aac aga 6768

Val Lys Arg Val Val Phe Gly Asp Ile Arg Ser His Ala Thr Asn Arg

2240

2245

2250

cat ttt ctt gct gcc agg gcg ctg cat tcg ctg ggc tcc aag gcg acc 6816

His Phe Leu Ala Ala Arg Ala Leu His Ser Leu Gly Ser Lys Ala Thr

2255

2260

2265

aaa gat gct ata cgt caa aag atg acg gag atg gaa gag cgc gag gaa 6864

Lys Asp Ala Ile Arg Gln Lys Met Thr Glu Met Glu Glu Arg Glu Glu

2270

2275

2280

gag ctg ctc gtc gac ccg gcc ttc ttc acg gcg ctg ctg cag ggc cag 6912

Glu Leu Leu Val Asp Pro Ala Phe Phe Thr Ala Leu Leu Gln Gly Gln

2285

2290

2295

2300

ctt gcc gat cga atc aag cac gtc gag atc ctc ccg aag aac atg cgc 6960

Leu Ala Asp Arg Ile Lys His Val Glu Ile Leu Pro Lys Asn Met Arg

2305	2310	2315	
gcc acg aac gag ctg agc gcg tac cgg tat aca gcc gtc att cac gta			7008
Ala Thr Asn Glu Leu Ser Ala Tyr Arg Tyr Thr Ala Val Ile His Val			
2320	2325	2330	
cgc ggc cca gag gaa cag tcg cgg ccc gtg tat ccg atc caa gtg aac			7056
Arg Gly Pro Glu Glu Gln Ser Arg Pro Val Tyr Pro Ile Gln Val Asn			
2335	2340	2345	
gac tgg atc gac ttt cag gcc tca cgc att gac cgc cgc gcc ctt ctc			7104
Asp Trp Ile Asp Phe Gln Ala Ser Arg Ile Asp Arg Arg Ala Leu Leu			
2350	2355	2360	
cga ctc cta cag cgc tcg gca gac gcc gcg acc gtc gcc gtc agc aac			7152
Arg Leu Leu Gln Arg Ser Ala Asp Ala Ala Thr Val Ala Val Ser Asn			
2365	2370	2375	2380
atc ccc tac agc aag acg att gta gaa cgc cat gtc gtc gag tcc ctt			7200
Ile Pro Tyr Ser Lys Thr Ile Val Glu Arg His Val Val Glu Ser Leu			
2385	2390	2395	
gac aat aac aac agg gag aat acg cat aga gca cca gac ggc gcg gct			7248
Asp Asn Asn Asn Arg Glu Asn Thr His Arg Ala Pro Asp Gly Ala Ala			
2400	2405	2410	
tgg atc tcg gcc gtc cgc tcc aag gcc gag cgc tgc acg tcc ctc tcc			7296
Trp Ile Ser Ala Val Arg Ser Lys Ala Glu Arg Cys Thr Ser Leu Ser			
2415	2420	2425	

gtg acc gat ctt gtg cag ctc ggg gaa gaa gcc ggc ttt cgc gta gaa 7344  
Val Thr Asp Leu Val Gln Leu Gly Glu Glu Ala Gly Phe Arg Val Glu  
2430 2435 2440

gtc agc gca gcg cgg cag tgg tct caa agc ggc gcg ctc gat gcc gtc 7392  
Val Ser Ala Ala Arg Gln Trp Ser Gln Ser Gly Ala Leu Asp Ala Val  
2445 2450 2455 2460

ttt cac cgc tat aat ttg ccc act caa agc aat agt cgc gtt ctg att 7440  
Phe His Arg Tyr Asn Leu Pro Thr Gln Ser Asn Ser Arg Val Leu Ile  
2465 2470 2475

cag ttc cct acc gaa gat ggc cag acg cga aga tcc gcc act ctg aca 7488  
Gln Phe Pro Thr Glu Asp Gly Gln Thr Arg Arg Ser Ala Thr Leu Thr  
2480 2485 2490

aac cga cca cta cag cgt ctg cag agc cgt cgg ttc gca tca cag atc 7536  
Asn Arg Pro Leu Gln Arg Leu Gln Ser Arg Arg Phe Ala Ser Gln Ile  
2495 2500 2505

cgc gaa cag ctg aag gcc gtg ctc ccg tca tac atg atc ccc tcc cgc 7584  
Arg Glu Gln Leu Lys Ala Val Leu Pro Ser Tyr Met Ile Pro Ser Arg  
2510 2515 2520

atc gtg gtc ata gac cag atg cct ctc aat gcc aat ggc aag gtc gac 7632  
Ile Val Val Ile Asp Gln Met Pro Leu Asn Ala Asn Gly Lys Val Asp  
2525 2530 2535 2540

cg~~g~~ aaa gaa c~~t~~ acc aga agg gcc caa atc gc~~g~~ cc~~g~~ aaa t~~c~~ t~~c~~ c~~g~~ g~~c~~ 7680  
Arg Lys Glu Leu Thr Arg Arg Ala Gln Ile Ala Pro Lys Ser Gln Ala

2545 2550 2555

g~~c~~ t ccc g~~c~~ c~~a~~ a~~a~~ ccc g~~t~~ c~~a~~ a~~a~~ c~~a~~ g~~t~~ g~~t~~ g~~a~~ t~~c~~ c~~g~~ a~~a~~ c~~t~~ g~~a~~ 7728  
Ala Pro Ala Lys Pro Val Lys Gln Val Asp Pro Phe Val Asn Leu Glu

2560 2565 2570

g~~c~~ c~~a~~ t t~~a~~ t~~g~~ t~~g~~ g~~a~~ g~~a~~ g~~t~~ c~~g~~ g~~a~~ g~~t~~ c~~t~~ g~~g~~ a~~t~~ g~~a~~ g~~t~~ g~~c~~ 7776  
Ala Ile Leu Cys Glu Glu Phe Ala Glu Val Leu Gly Met Glu Val Gly

2575 2580 2585

g~~t~~ g~~a~~ a~~a~~ g~~a~~ c~~a~~ c~~a~~ t~~t~~ c~~t~~ c~~a~~ a~~a~~ c~~t~~ g~~c~~ c~~t~~ t~~t~~ g~~c~~ a~~c~~ 7824  
Val Asn Asp His Phe Phe Gln Leu Gly Gly His Ser Leu Leu Ala Thr

2590 2595 2600

a~~a~~ g~~c~~ t~~c~~ g~~t~~ c~~g~~ c~~g~~ t~~c~~ a~~g~~ t~~c~~ c~~g~~ g~~t~~ c~~a~~ a~~a~~ g~~g~~ t~~c~~ c~~g~~ t~~t~~ g~~t~~ 7872  
Lys Leu Val Ala Arg Leu Ser Arg Arg Leu Asn Gly Arg Val Ser Val  
2605 2610 2615 2620

agg g~~a~~ t~~t~~ g~~t~~ g~~a~~ c~~a~~ c~~a~~ g~~c~~ t~~c~~ g~~t~~ a~~t~~ t~~c~~ g~~a~~ c~~t~~ c~~g~~ a~~c~~ c~~t~~ 7920  
Arg Asp Val Phe Asp Gln Pro Val Ile Ser Asp Leu Ala Val Thr Leu  
2625 2630 2635

c~~g~~ c~~a~~ g~~g~~ a~~c~~ t~~t~~ g~~a~~ a~~a~~ g~~c~~ a~~t~~ t~~c~~ c~~g~~ a~~c~~ g~~a~~ a~~c~~ 7968  
Arg Gln Gly Leu Thr Leu Glu Asn Ala Ile Pro Ala Thr Pro Asp Ser  
2640 2645 2650

g~~g~~ g~~t~~ a~~t~~ t~~g~~ g~~a~~ c~~a~~ a~~t~~ g~~t~~ g~~c~~ a~~c~~ a~~a~~ c~~c~~ g~~a~~ g~~c~~ g~~a~~ c~~a~~ 8016

Gly Tyr Trp Glu Gln Thr Met Ser Ala Pro Thr Thr Pro Ser Asp Asp

2655

2660

2665

atg gag gcc gtg cta tgc aag gag ttt gcg gat gtg ctt ggc gtc gaa 8064

Met Glu Ala Val Leu Cys Lys Glu Phe Ala Asp Val Leu Gly Val Glu

2670

2675

2680

gtc agc gcc acc gac agc ttc ttc gat ctc ggt ggg cat tcc ctc atg 8112

Val Ser Ala Thr Asp Ser Phe Phe Asp Leu Gly Gly His Ser Leu Met

2685

2690

2695

2700

gct acg aag ctc gct gcg cgt att agc cgt cgg cta gat gta ccg gtg 8160

Ala Thr Lys Leu Ala Ala Arg Ile Ser Arg Arg Leu Asp Val Pro Val

2705

2710

2715

tca atc aaa gac ata ttc gat cac tca gtt cct cta aac ctt gcg agg 8208

Ser Ile Lys Asp Ile Phe Asp His Ser Val Pro Leu Asn Leu Ala Arg

2720

2725

2730

aag att cgg ctc actcaa gca aaa ggc cac gaa gcg acc aat gga gta 8256

Lys Ile Arg Leu Thr Gln Ala Lys Gly His Glu Ala Thr Asn Gly Val

2735

2740

2745

caa atc gcc aac gac gcc cca ttc caa ctc att tcc gta gaa gat cca 8304

Gln Ile Ala Asn Asp Ala Pro Phe Gln Leu Ile Ser Val Glu Asp Pro

2750

2755

2760

gag ata ttc gtc caa cgt gaa atc gcc cct caa cta caa tgc tca ccc 8352

Glu Ile Phe Val Gln Arg Glu Ile Ala Pro Gln Leu Gln Cys Ser Pro

2765

2770

2775

2780

gag aca atc cta gac gtc tac ccc gcc acg caa atg caa agg gtc ttc 8400  
Glu Thr Ile Leu Asp Val Tyr Pro Ala Thr Gln Met Gln Arg Val Phe

2785

2790

2795

ctc ctc aac cca gta aca gga aag ccg cgc tca cca acg cca ttt cac 8448  
Leu Leu Asn Pro Val Thr Gly Lys Pro Arg Ser Pro Thr Pro Phe His

2800

2805

2810

ata gac ttc ccg ccg gac gca gac tgc gcc agc ctg atg cgg gca tgt 8496  
Ile Asp Phe Pro Pro Asp Ala Asp Cys Ala Ser Leu Met Arg Ala Cys

2815

2820

2825

gca tct cta gcg aag cat ttc gat atc ttc agg acg gtg ttc ctc gaa 8544  
Ala Ser Leu Ala Lys His Phe Asp Ile Phe Arg Thr Val Phe Leu Glu

2830

2835

2840

gcc aga ggc gaa ctc tac caa gta gtt cta aaa cac gtc gac gtg ccc 8592  
Ala Arg Gly Glu Leu Tyr Gln Val Val Leu Lys His Val Asp Val Pro  
2845 2850 2855 2860

atc gag atg ctc cag acc gaa gaa aac atc aac agc gcg acc cgg tcg 8640  
Ile Glu Met Leu Gln Thr Glu Glu Asn Ile Asn Ser Ala Thr Arg Ser  
2865 2870 2875

ttc ctg gac gta gac gca gaa aaa ccc atc cgg cta ggc cag cca ctg 8688  
Phe Leu Asp Val Asp Ala Glu Lys Pro Ile Arg Leu Gly Gln Pro Leu  
2880 2885 2890

atc cgc atc gcg ata cta gag aag ccc ggg tcc acg ctg cgc gtc atc 8736  
Ile Arg Ile Ala Ile Leu Glu Lys Pro Gly Ser Thr Leu Arg Val Ile  
2895 2900 2905

cta cga tta tcc cac gcc tta tac gac ggc ctg agc cta gag cac atc 8784  
Leu Arg Leu Ser His Ala Leu Tyr Asp Gly Leu Ser Leu Glu His Ile  
2910 2915 2920

ctg cac tct ctg cac atc ctc ttt ttc ggc ggc agt ctt ccc ccg ccg 8832  
Leu His Ser Leu His Ile Leu Phe Phe Gly Gly Ser Leu Pro Pro Pro  
2925 2930 2935 2940

ccc aag ttc gcc ggg tac atg caa cac gtc gcg agc agt cgc aga gaa 8880  
Pro Lys Phe Ala Gly Tyr Met Gln His Val Ala Ser Ser Arg Arg Glu  
2945 2950 2955

ggc tac gat ttc tgg cgt tcc gtt ctc cga gat tcg tct atg aca gtc 8928  
Gly Tyr Asp Phe Trp Arg Ser Val Leu Arg Asp Ser Ser Met Thr Val  
2960 2965 2970

atc aaa ggc aac aat aat aca act cca cca cct cct cct caa caa caa 8976  
Ile Lys Gly Asn Asn Asn Thr Thr Pro Pro Pro Pro Gln Gln Gln  
2975 2980 2985

tcc acc ccc tcc gga gcc cac cac gcc tcc aaa gta gtc act atc cca 9024  
Ser Thr Pro Ser Gly Ala His His Ala Ser Lys Val Val Thr Ile Pro  
2990 2995 3000

acc caa gcc aac aca gac agc cg<sub>g</sub> atc acg cgc gcc acg atc ttc act 9072  
Thr Gln Ala Asn Thr Asp Ser Arg Ile Thr Arg Ala Thr Ile Phe Thr  
3005 3010 3015 3020

acc gct tgc gca cta atg ctc gc<sub>g</sub> aaa gaa gac aac tcc acg gac gtc 9120  
Thr Ala Cys Ala Leu Met Leu Ala Lys Glu Asp Asn Ser Ser Asp Val  
3025 3030 3035

gtc ttc ggg cgt acg gta tc<sub>g</sub> ggg cgt caa ggc ctg ccc cta gcc cac 9168  
Val Phe Gly Arg Thr Val Ser Gly Arg Gln Gly Leu Pro Leu Ala His  
3040 3045 3050

caa aac gt<sub>g</sub> atc gga cca tgt ctc aac caa gt<sub>g</sub> ccc gt<sub>g</sub> cgc gc<sub>g</sub> cgc 9216  
Gln Asn Val Ile Gly Pro Cys Leu Asn Gln Val Pro Val Arg Ala Arg  
3055 3060 3065

gg<sub>t</sub> tta aac cga gga acc act cac cac cga gaa ctt ctc cgc gag atg 9264  
Gly Leu Asn Arg Gly Thr Thr His His Arg Glu Leu Leu Arg Glu Met  
3070 3075 3080

caa gag caa tat ctc aac agt ctc gct ttc gaa act ctc ggg tac gac 9312  
Gln Glu Gln Tyr Leu Asn Ser Leu Ala Phe Glu Thr Leu Gly Tyr Asp  
3085 3090 3095 3100

gag atc aag gc<sub>g</sub> cac tgc aca gac tgg cc<sub>g</sub> gac gt<sub>g</sub> cca gc<sub>g</sub> acc gc<sub>g</sub> 9360  
Glu Ile Lys Ala His Cys Thr Asp Trp Pro Asp Val Pro Ala Thr Ala  
3105 3110 3115

agc ttc ggg tgc tgc atc gt<sub>g</sub> tac cag aac ttc gat tc<sub>g</sub> cac cc<sub>g</sub> gac 9408

Ser Phe Gly Cys Cys Ile Val Tyr Gln Asn Phe Asp Ser His Pro Asp  
3120 3125 3130

agc cga gtc gaa gag cag cggtc cag atc ggg gtc ttg tcg cggtc aac 9456  
Ser Arg Val Glu Glu Gln Arg Leu Gln Ile Gly Val Leu Ser Arg Asn  
3135 3140 3145

tcg gag gct att aat gag ggg ctc gtg cat gat ctt gtt att gct ggg 9504  
Tyr Glu Ala Ile Asn Glu Gly Leu Val His Asp Leu Val Ile Ala Gly  
3150 3155 3160

gag tcg gag cct gat ggg gat gat ttg agg gtt act gtt gtg gcg aat 9552  
Glu Ser Glu Pro Asp Gly Asp Asp Leu Arg Val Thr Val Val Ala Asn  
3165 3170 3175 3180

cggtc agg ttg tgc gat gag gaa agg ttg aag agg atg ctg gag gag ctg 9600  
Arg Arg Leu Cys Asp Glu Glu Arg Leu Lys Arg Met Leu Glu Glu Leu  
3185 3190 3195

tgt ggg aat att cggtc gct ttg gcg ttg gtt tag 9633  
Cys Gly Asn Ile Arg Ala Leu Ala Leu Val  
3200 3205

<210> 2

<211> 3210

<212> PRT

<213> Mycelia sterilia

<400> 2

Met Ser Asn Met Ala Pro Leu Pro Thr Met Gly Val Glu Gln Gln Ala

1

5

10

15

Leu Ser Leu Ser Cys Pro Leu Leu Pro His Asp Asp Glu Lys His Ser

20

25

30

Asp Asn Leu Tyr Glu Gln Ala Thr Arg His Phe Gly Leu Ser Arg Asp

35

40

45

Lys Ile Glu Asn Val Leu Pro Cys Thr Ser Phe Gln Cys Asp Val Ile

50

55

60

Asp Cys Ala Val Asp Asp Arg Arg His Ala Ile Gly His Val Val Tyr

65

70

75

80

Asp Ile Pro Asn Thr Val Asp Ile Gln Arg Leu Ala Ala Ala Trp Lys

85

90

95

Glu Val Val Arg Gln Thr Pro Ile Leu Arg Thr Gly Ile Phe Thr Ser

100

105

110

Glu Thr Gly Asp Ser Phe Gln Ile Val Leu Lys Glu Gly Cys Leu Pro

115

120

125

Trp Met Tyr Ala Thr Cys Leu Gly Met Lys Gly Ala Val Ile Gln Asp

130

135

140

Glu Ala Val Ala Ala Met Thr Gly Pro Arg Cys Asn Arg Tyr Val Val

145

150

155

160

Leu Glu Asp Pro Ser Thr Lys Gln Arg Leu Leu Ile Trp Thr Phe Ser

165

170

175

His Ala Leu Val Asp Tyr Thr Val Gln Glu Arg Ile Leu Gln Arg Val

180

185

190

Leu Thr Val Tyr Asp Gly Arg Asp Val Glu Cys Pro Arg Ile Lys Asp

195

200

205

Thr Glu His Val Ser Arg Phe Trp Gln Gln His Phe Glu Gly Leu Asp

210

215

220

Ala Ser Val Phe Pro Leu Leu Pro Ser His Leu Thr Val Cys Asn Pro

225

230

235

240

Asn Ala Arg Ala Glu His His Ile Ser Tyr Thr Gly Pro Val Gln Arg

245

250

255

Lys Trp Ser His Thr Ser Ile Cys Arg Ala Ala Leu Ala Val Leu Leu

260

265

270

Ser Arg Phe Thr His Ser Ser Glu Ala Leu Phe Gly Val Val Thr Glu

275

280

285

Gln Ser His Asn Ser Glu Asp Gln Arg Arg Ser Ile Asp Gly Pro Ala

290

295

300

Arg Thr Val Val Pro Ile Arg Val Leu Cys Ala Pro Asp Gln Tyr Val  
305 310 315 320

Ser Asp Val Ile Gly Ala Ile Thr Ala His Glu His Ala Met Arg Gly  
325 330 335

Phe Glu His Ala Gly Leu Arg Asn Ile Arg Arg Thr Gly Asp Asp Gly  
340 345 350

Ser Ala Ala Cys Gly Phe Gln Thr Val Leu Leu Val Thr Asp Gly Asp  
355 360 365

Ala Pro Lys Thr Pro Gly Ser Val Leu His Arg Ser Val Glu Glu Ser  
370 375 380

Asp Arg Phe Met Pro Cys Ala Asn Arg Ala Leu Leu Asp Cys Gln  
385 390 395 400

Met Ala Gly Asn Ser Ala Ser Leu Val Ala Arg Tyr Asp His Asn Val  
405 410 415

Ile Asp Pro Arg Gln Met Ser Arg Phe Leu Arg Gln Leu Gly Tyr Leu  
420 425 430

Ile Gln Gln Phe His His His Val Asp Leu Pro Leu Val Lys Glu Leu  
435 440 445

Asp Val Val Thr Ala Glu Asp Cys Ala Glu Ile Glu Lys Trp Asn Ser  
450 455 460

Glu Arg Leu Thr Met Gln Asp Ala Leu Ile His Asp Thr Ile Ser Lys  
465 470 475 480

Trp Ala Ala Gly Asp Pro Asn Lys Ala Ala Val Phe Ala Trp Asp Gly  
485 490 495

Glu Trp Thr Tyr Ala Glu Leu Asp Asn Ile Ser Ser Arg Leu Ala Val  
500 505 510

Tyr Ile Gln Ser Leu Asp Leu Arg Pro Gly Gln Ala Ile Leu Pro Leu  
515 520 525

Cys Phe Glu Lys Ser Lys Trp Val Val Ala Thr Ile Leu Ala Val Leu  
530 535 540

Lys Val Gly Arg Ala Phe Thr Leu Ile Asp Pro Cys Asp Pro Ser Ala  
545 550 555 560

Arg Met Ala Gln Val Cys Gln Gln Thr Ser Ala Thr Val Ala Leu Thr  
565 570 575

Ser Lys Leu His Asn Thr Thr Leu Arg Ser Val Val Ser Arg Cys Ile  
580 585 590

Val Val Asp Asp Asp Leu Leu Arg Ser Leu Pro His Ala Asp Gly Arg  
595 600 605

Leu Lys Ala Thr Val Lys Pro Gln Asp Leu Ala Tyr Val Ile Phe Thr

610

615

620

Ser Gly Ser Thr Gly Glu Pro Lys Gly Ile Met Ile Glu His Arg Gly

625

630

635

640

Phe Val Ser Cys Ala Met Lys Phe Gly Pro Ala Leu Gly Met Asp Glu

645

650

655

His Thr Arg Ala Leu Gln Phe Ala Ser Tyr Ala Phe Gly Ala Cys Leu

660

665

670

Val Glu Val Val Thr Ala Leu Met His Gly Gly Cys Val Cys Ile Pro

675

680

685

Ser Asp Asp Asp Arg Leu Asn Asn Val Pro Glu Phe Ile Lys Arg Ala

690

695

700

Gln Val Asn Trp Val Ile Leu Thr Pro Ser Tyr Ile Gly Thr Phe Gln

705

710

715

720

Pro Glu Asp Val Pro Gly Leu Gln Thr Leu Val Leu Val Gly Glu Pro

725

730

735

Ile Ser Ala Ser Ile Arg Asp Thr Trp Ala Ser Gln Val Arg Leu Leu

740

745

750

Asn Ala Tyr Gly Gln Ser Glu Ser Ser Thr Met Cys Ser Val Thr Glu

755

760

765

Val Ser Pro Leu Ser Leu Glu Pro Asn Asn Ile Gly Arg Ala Val Gly  
770 775 780

Ala Arg Ser Trp Ile Ile Asp Pro Asp Glu Pro Asp Arg Leu Ala Pro  
785 790 795 800

Ile Gly Cys Ile Gly Glu Leu Val Ile Glu Ser Pro Gly Ile Ala Arg  
805 810 815

Asp Tyr Ile Ile Ala Pro Pro Pro Asp Lys Ser Pro Phe Leu Leu Ala  
820 825 830

Pro Pro Ala Trp Tyr Pro Ala Gly Lys Leu Ser Asn Ala Phe Lys Phe  
835 840 845

Tyr Lys Thr Gly Asp Leu Val Arg Tyr Gly Pro Asp Gly Thr Ile Val  
850 855 860

Cys Leu Gly Arg Lys Asp Ser Gln Val Lys Ile Arg Gly Gln Arg Val  
865 870 875 880

Glu Ile Ser Ala Val Glu Ala Ser Leu Arg Arg Gln Leu Pro Ser Asp  
885 890 895

Ile Met Pro Val Ala Glu Ala Ile Lys Arg Ser Asp Ser Ser Gly Ser  
900 905 910

Thr Val Leu Thr Ala Phe Leu Ile Gly Ser Ser Lys Ser Gly Asp Gly

915

920

925

Asn Gly His Ala Leu Ser Ala Ala Asp Ala Val Ile Leu Asp His Gly

930

935

940

Ala Thr Asn Glu Ile Asn Ala Lys Leu Gln Gln Ile Leu Pro Gln His

945

950

955

960

Ser Val Pro Ser Tyr Tyr Ile His Met Glu Asn Leu Pro Arg Thr Ala

965

970

975

Thr Gly Lys Ala Asp Arg Lys Met Leu Arg Ser Ile Ala Ser Lys Leu

980

985

990

Leu Gly Glu Leu Ser Gln Asn Val Thr Ser Gln Pro Ile Glu Lys His

995

1000

1005

Asp Ala Pro Ala Thr Gly Ile Glu Val Lys Leu Lys Glu Leu Trp Phe

1010

1015

1020

Leu Ser Leu Asn Leu Asn Pro Asn Ser Gln Asp Val Gly Ala Ser Phe

1025

1030

1035

1040

Phe Asp Leu Gly Gly Asn Ser Ile Ile Ala Ile Lys Met Val Asn Met

1045

1050

1055

Ala Arg Ser Ala Gly Ile Ala Leu Lys Val Ser Asp Ile Phe Gln Asn

1060

1065

1070

Pro Thr Leu Ala Gly Leu Val Asp Val Ile Gly Arg Asp Pro Ala Pro  
1075 1080 1085

Tyr Asn Leu Ile Pro Thr Thr Ala Tyr Ser Gly Pro Val Glu Gln Ser  
1090 1095 1100

Phe Ala Gln Gly Arg Leu Trp Phe Leu Asp Gln Ile Glu Leu Asp Ala  
105 1110 1115 1120

Leu Trp Tyr Leu Leu Pro Tyr Ala Val Arg Met Arg Gly Pro Leu His  
1125 1130 1135

Ile Asp Ala Leu Thr Ile Ala Leu Leu Ala Ile Gln Gln Arg His Glu  
1140 1145 1150

Thr Leu Arg Thr Thr Phe Glu Glu Gln Asp Gly Val Gly Val Gln Val  
1155 1160 1165

Val His Ala Ser Pro Ile Ser Asp Leu Arg Ile Ile Asp Val Ser Gly  
1170 1175 1180

Asp Arg Asn Ser Asp Tyr Leu Gln Leu His Gln Glu Gln Thr Thr  
185 1190 1195 1200

Pro Phe Ile Leu Ala Cys Gln Ala Gly Trp Arg Val Ser Leu Ile Arg  
1205 1210 1215

Leu Gly Glu Asp Asp His Ile Leu Ser Ile Val Met His His Ile Ile  
1220 1225 1230

Ser Asp Gly Trp Ser Ile Asp Ile Leu Arg Arg Glu Leu Ser Asn Phe  
1235 1240 1245

Tyr Ser Ala Ala Leu Arg Gly Ser Asp Pro Leu Ser Val Val Ser Pro  
1250 1255 1260

Leu Pro Leu His Tyr Arg Asp Phe Ser Val Trp Gln Lys Gln Val Glu  
265 1270 1275 1280

Gln Glu Thr Glu His Glu Arg Gln Leu Glu Tyr Trp Val Lys Gln Leu  
1285 1290 1295

Ala Asp Ser Ser Ala Ala Glu Phe Leu Thr Asp Phe Pro Arg Pro Asn  
1300 1305 1310

Ile Leu Ser Gly Glu Ala Gly Ser Val Pro Val Thr Ile Glu Gly Glu  
1315 1320 1325

Leu Tyr Glu Arg Leu Gln Glu Phe Cys Lys Val Glu Gln Met Thr Pro  
1330 1335 1340

Phe Ala Val Leu Leu Gly Ala Phe Arg Ala Thr His Tyr Arg Leu Thr  
345 1350 1355 1360

Gly Ala Glu Asp Ser Ile Ile Gly Thr Pro Ile Ala Asn Arg Asn Arg  
1365 1370 1375

Gln Glu Leu Glu Asn Met Ile Gly Phe Phe Val Asn Thr Gln Cys Met

1380

1385

1390

Arg Ile Thr Val Asp Gly Asp Asp Thr Phe Glu Ser Leu Val Arg Gln

1395

1400

1405

Val Arg Thr Thr Ala Thr Ala Ala Phe Glu His Gln Asp Val Pro Phe

1410

1415

1420

Glu Arg Val Val Thr Ala Leu Leu Pro Arg Ser Arg Asp Leu Ser Arg

425

1430

1435

1440

Asn Pro Leu Ala Gln Leu Thr Phe Ala Leu His Ser Gln Gln Asp Leu

1445

1450

1455

Gly Lys Phe Glu Leu Glu Gly Leu Val Ala Glu Pro Val Ser Asn Lys

1460

1465

1470

Val Tyr Thr Arg Phe Asp Val Glu Phe His Leu Phe Gln Glu Ala Gly

1475

1480

1485

Arg Leu Ser Gly Asn Val Ala Phe Ala Ala Asp Leu Phe Lys Pro Glu

1490

1495

1500

Thr Ile Ser Asn Val Val Ala Ile Phe Phe Gln Ile Leu Arg Gln Gly

505

1510

1515

1520

Ile Arg Gln Pro Arg Thr Pro Ile Ala Val Leu Pro Leu Thr Asp Gly

1525

1530

1535

Leu Ala Asp Leu Arg Ala Met Gly Leu Leu Glu Ile Glu Lys Ala Glu

1540

1545

1550

Tyr Pro Arg Glu Ser Ser Val Val Asp Val Phe Arg Lys Gln Val Ala

1555

1560

1565

Ala His Pro His Ala Phe Ala Val Val Asp Ser Ala Ser Arg Leu Thr

1570

1575

1580

Tyr Ala Asp Leu Asp Arg Gln Ser Asp Gln Leu Ala Thr Trp Leu Gly

585

1590

1595

1600

Arg Arg Asn Met Thr Ala Glu Thr Leu Val Gly Val Leu Ala Pro Arg

1605

1610

1615

Ser Cys Gln Thr Val Val Ala Ile Leu Gly Ile Leu Lys Ala Asn Leu

1620

1625

1630

Ala Tyr Leu Pro Leu Asp Val Asn Cys Pro Thr Ala Arg Leu Gln Thr

1635

1640

1645

Ile Leu Ser Thr Leu Asn Arg His Lys Leu Val Leu Leu Gly Ser Asn

1650

1655

1660

Ala Thr Thr Pro Asp Val Gln Ile Pro Asp Val Glu Leu Val Arg Ile

665

1670

1675

1680

Ser Asp Ile Leu Asp Arg Pro Ile Asn Gly Gln Ala Lys Leu Asn Gly

1685

1690

1695

His Thr Lys Ser Asn Gly Tyr Ser Lys Pro Asn Gly Tyr Thr His Leu  
1700 1705 1710

Lys Gly Tyr Ser Asn Leu Asn Gly Tyr Ser Lys Gln Asn Gly Tyr Ala  
1715 1720 1725

Gln Leu Asn Gly His Arg Glu Arg Asn Asn Tyr Leu Asp Leu Asn Gly  
1730 1735 1740

His Ser Leu Leu Asn Gly Asn Ser Asp Ile Thr Thr Ser Gly Pro Ser  
745 1750 1755 1760

Ala Thr Ser Leu Ala Tyr Val Ile Phe Thr Ser Gly Ser Thr Gly Lys  
1765 1770 1775

Pro Lys Gly Val Met Val Glu His Arg Ser Ile Ile Arg Leu Ala Lys  
1780 1785 1790

Lys Asn Arg Ile Ile Ser Arg Phe Pro Ser Val Ala Lys Val Ala His  
1795 1800 1805

Leu Ser Asn Ile Ala Phe Asp Ala Ala Thr Trp Glu Met Phe Ala Ala  
1810 1815 1820

Leu Leu Asn Gly Gly Thr Leu Val Cys Ile Asp Tyr Met Thr Thr Leu  
825 1830 1835 1840

Asp Ser Lys Thr Leu Glu Ala Ala Phe Ala Arg Glu Gln Ile Asn Ala

1845

1850

1855

Ala Leu Leu Thr Pro Ala Leu Leu Lys Gln Cys Leu Ala Asn Ile Pro

1860

1865

1870

Thr Thr Leu Gly Arg Leu Ser Ala Leu Val Ile Gly Gly Asp Arg Leu

1875

1880

1885

Asp Gly Gln Asp Ala Ile Ala Ala His Ala Leu Val Gly Ala Gly Val

1890

1895

1900

Tyr Asn Ala Tyr Gly Pro Thr Glu Asn Gly Val Ile Ser Thr Ile Tyr

905

1910

1915

1920

Asn Ile Thr Lys Asn Asp Ser Phe Ile Asn Gly Val Pro Ile Gly Cys

1925

1930

1935

Ala Ile Ser Asn Ser Gly Ala Tyr Ile Thr Asp Pro Asp Gln Gln Leu

1940

1945

1950

Val Pro Pro Gly Val Met Gly Glu Leu Val Val Thr Gly Asp Gly Leu

1955

1960

1965

Ala Arg Gly Tyr Thr Asp Pro Ala Leu Asp Ala Gly Arg Phe Val Gln

1970

1975

1980

Ile Met Ile Asn Asp Lys Ala Val Arg Ala Tyr Arg Thr Gly Asp Arg

985

1990

1995

2000

Ala Arg Tyr Arg Val Gly Asp Gly Gln Ile Glu Phe Phe Gly Arg Met

2005

2010

2015

Asp Gln Gln Val Lys Ile Arg Gly His Arg Ile Glu Pro Ala Glu Val

2020

2025

2030

Glu Arg Ala Ile Leu Asp Gln Asp Ser Ala Arg Asp Ala Val Val Val

2035

2040

2045

Ile Arg His Gln Glu Gly Glu Glu Pro Glu Met Val Gly Phe Val Ala

2050

2055

2060

Thr His Gly Asp His Ser Ala Glu Gln Glu Glu Ala Asp Asp Gln Val

065

2070

2075

2080

Glu Gly Trp Lys Asp Phe Phe Glu Ser Asn Thr Tyr Ala Asp Met Asp

2085

2090

2095

Thr Ile Gly Gln Ser Ala Ile Gly Asn Asp Phe Thr Gly Trp Thr Ser

2100

2105

2110

Met Tyr Asp Gly Ser Glu Ile Asn Lys Ala Glu Met Gln Glu Trp Leu

2115

2120

2125

Asp Asp Thr Met Arg Thr Leu Leu Asp Gly Gln Ala Pro Gly His Val

2130

2135

2140

Leu Glu Ile Gly Thr Gly Ser Gly Met Val Leu Phe Asn Leu Gly Ala

145

2150

2155

2160

Gly Leu Gln Ser Tyr Val Gly Leu Glu Pro Ser Arg Ser Ala Ala Thr  
2165 2170 2175

Phe Val Thr Lys Ala Ile Asn Ser Thr Pro Ala Leu Ala Gly Lys Ala  
2180 2185 2190

Glu Val His Val Gly Thr Ala Thr Asp Ile Asn Arg Leu Arg Gly Leu  
2195 2200 2205

Arg Pro Asp Leu Val Val Leu Asn Ser Val Val Gln Tyr Phe Pro Thr  
2210 2215 2220

Pro Glu Tyr Leu Leu Glu Val Val Glu Ser Leu Val Arg Ile Pro Gly  
225 2230 2235 2240

Val Lys Arg Val Val Phe Gly Asp Ile Arg Ser His Ala Thr Asn Arg  
2245 2250 2255

His Phe Leu Ala Ala Arg Ala Leu His Ser Leu Gly Ser Lys Ala Thr  
2260 2265 2270

Lys Asp Ala Ile Arg Gln Lys Met Thr Glu Met Glu Glu Arg Glu Glu  
2275 2280 2285

Glu Leu Leu Val Asp Pro Ala Phe Phe Thr Ala Leu Leu Gln Gly Gln  
2290 2295 2300

Leu Ala Asp Arg Ile Lys His Val Glu Ile Leu Pro Lys Asn Met Arg

305

2310

2315

2320

Ala Thr Asn Glu Leu Ser Ala Tyr Arg Tyr Thr Ala Val Ile His Val

2325

2330

2335

Arg Gly Pro Glu Glu Gln Ser Arg Pro Val Tyr Pro Ile Gln Val Asn

2340

2345

2350

Asp Trp Ile Asp Phe Gln Ala Ser Arg Ile Asp Arg Arg Ala Leu Leu

2355

2360

2365

Arg Leu Leu Gln Arg Ser Ala Asp Ala Ala Thr Val Ala Val Ser Asn

2370

2375

2380

Ile Pro Tyr Ser Lys Thr Ile Val Glu Arg His Val Val Glu Ser Leu

385

2390

2395

2400

Asp Asn Asn Asn Arg Glu Asn Thr His Arg Ala Pro Asp Gly Ala Ala

2405

2410

2415

Trp Ile Ser Ala Val Arg Ser Lys Ala Glu Arg Cys Thr Ser Leu Ser

2420

2425

2430

Val Thr Asp Leu Val Gln Leu Gly Glu Glu Ala Gly Phe Arg Val Glu

2435

2440

2445

Val Ser Ala Ala Arg Gln Trp Ser Gln Ser Gly Ala Leu Asp Ala Val

2450

2455

2460

Phe His Arg Tyr Asn Leu Pro Thr Gln Ser Asn Ser Arg Val Leu Ile  
465 2470 2475 2480

Gln Phe Pro Thr Glu Asp Gly Gln Thr Arg Arg Ser Ala Thr Leu Thr  
2485 2490 2495

Asn Arg Pro Leu Gln Arg Leu Gln Ser Arg Arg Phe Ala Ser Gln Ile  
2500 2505 2510

Arg Glu Gln Leu Lys Ala Val Leu Pro Ser Tyr Met Ile Pro Ser Arg  
2515 2520 2525

Ile Val Val Ile Asp Gln Met Pro Leu Asn Ala Asn Gly Lys Val Asp  
2530 2535 2540

Arg Lys Glu Leu Thr Arg Arg Ala Gln Ile Ala Pro Lys Ser Gln Ala  
545 2550 2555 2560

Ala Pro Ala Lys Pro Val Lys Gln Val Asp Pro Phe Val Asn Leu Glu  
2565 2570 2575

Ala Ile Leu Cys Glu Glu Phe Ala Glu Val Leu Gly Met Glu Val Gly  
2580 2585 2590

Val Asn Asp His Phe Phe Gln Leu Gly Gly His Ser Leu Leu Ala Thr  
2595 2600 2605

Lys Leu Val Ala Arg Leu Ser Arg Arg Leu Asn Gly Arg Val Ser Val  
2610 2615 2620

Arg Asp Val Phe Asp Gln Pro Val Ile Ser Asp Leu Ala Val Thr Leu  
625 2630 2635 2640

Arg Gln Gly Leu Thr Leu Glu Asn Ala Ile Pro Ala Thr Pro Asp Ser  
2645 2650 2655

Gly Tyr Trp Glu Gln Thr Met Ser Ala Pro Thr Thr Pro Ser Asp Asp  
2660 2665 2670

Met Glu Ala Val Leu Cys Lys Glu Phe Ala Asp Val Leu Gly Val Glu  
2675 2680 2685

Val Ser Ala Thr Asp Ser Phe Phe Asp Leu Gly Gly His Ser Leu Met  
2690 2695 2700

Ala Thr Lys Leu Ala Ala Arg Ile Ser Arg Arg Leu Asp Val Pro Val  
705 2710 2715 2720

Ser Ile Lys Asp Ile Phe Asp His Ser Val Pro Leu Asn Leu Ala Arg  
2725 2730 2735

Lys Ile Arg Leu Thr Gln Ala Lys Gly His Glu Ala Thr Asn Gly Val  
2740 2745 2750

Gln Ile Ala Asn Asp Ala Pro Phe Gln Leu Ile Ser Val Glu Asp Pro  
2755 2760 2765

Glu Ile Phe Val Gln Arg Glu Ile Ala Pro Gln Leu Gln Cys Ser Pro

2770

2775

2780

Glu Thr Ile Leu Asp Val Tyr Pro Ala Thr Gln Met Gln Arg Val Phe

785

2790

2795

2800

Leu Leu Asn Pro Val Thr Gly Lys Pro Arg Ser Pro Thr Pro Phe His

2805

2810

2815

Ile Asp Phe Pro Pro Asp Ala Asp Cys Ala Ser Leu Met Arg Ala Cys

2820

2825

2830

Ala Ser Leu Ala Lys His Phe Asp Ile Phe Arg Thr Val Phe Leu Glu

2835

2840

2845

Ala Arg Gly Glu Leu Tyr Gln Val Val Leu Lys His Val Asp Val Pro

2850

2855

2860

Ile Glu Met Leu Gln Thr Glu Glu Asn Ile Asn Ser Ala Thr Arg Ser

865

2870

2875

2880

Phe Leu Asp Val Asp Ala Glu Lys Pro Ile Arg Leu Gly Gln Pro Leu

2885

2890

2895

Ile Arg Ile Ala Ile Leu Glu Lys Pro Gly Ser Thr Leu Arg Val Ile

2900

2905

2910

Leu Arg Leu Ser His Ala Leu Tyr Asp Gly Leu Ser Leu Glu His Ile

2915

2920

2925

Leu His Ser Leu His Ile Leu Phe Phe Gly Gly Ser Leu Pro Pro Pro  
2930 2935 2940

Pro Lys Phe Ala Gly Tyr Met Gln His Val Ala Ser Ser Arg Arg Glu  
945 2950 2955 2960

Gly Tyr Asp Phe Trp Arg Ser Val Leu Arg Asp Ser Ser Met Thr Val  
2965 2970 2975

Ile Lys Gly Asn Asn Asn Thr Thr Pro Pro Pro Pro Gln Gln Gln  
2980 2985 2990

Ser Thr Pro Ser Gly Ala His His Ala Ser Lys Val Val Thr Ile Pro  
2995 3000 3005

Thr Gln Ala Asn Thr Asp Ser Arg Ile Thr Arg Ala Thr Ile Phe Thr  
3010 3015 3020

Thr Ala Cys Ala Leu Met Leu Ala Lys Glu Asp Asn Ser Ser Asp Val  
025 3030 3035 3040

Val Phe Gly Arg Thr Val Ser Gly Arg Gln Gly Leu Pro Leu Ala His  
3045 3050 3055

Gln Asn Val Ile Gly Pro Cys Leu Asn Gln Val Pro Val Arg Ala Arg  
3060 3065 3070

Gly Leu Asn Arg Gly Thr Thr His His Arg Glu Leu Leu Arg Glu Met  
3075 3080 3085

Gln Glu Gln Tyr Leu Asn Ser Leu Ala Phe Glu Thr Leu Gly Tyr Asp  
3090 3095 3100

Glu Ile Lys Ala His Cys Thr Asp Trp Pro Asp Val Pro Ala Thr Ala  
105 3110 3115 3120

Ser Phe Gly Cys Cys Ile Val Tyr Gln Asn Phe Asp Ser His Pro Asp  
3125 3130 3135

Ser Arg Val Glu Glu Gln Arg Leu Gln Ile Gly Val Leu Ser Arg Asn  
3140 3145 3150

Tyr Glu Ala Ile Asn Glu Gly Leu Val His Asp Leu Val Ile Ala Gly  
3155 3160 3165

Glu Ser Glu Pro Asp Gly Asp Asp Leu Arg Val Thr Val Val Ala Asn  
3170 3175 3180

Arg Arg Leu Cys Asp Glu Glu Arg Leu Lys Arg Met Leu Glu Glu Leu  
185 3190 3195 3200

Cys Gly Asn Ile Arg Ala Leu Ala Leu Val  
3205 3210

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 3

tggacnwsna tgtaygaygg

20

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 4

gtnggraart aytgnacnac

20

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 5

gcggaattaa ccctcactaa agggAACGAA

30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 6

gcgttaatacg actcactata gggcgaagaa

30

<210> 7

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 7

agcatcggtt cctaacaatg ggcgttggc agcaaggccct a

41

<210> 8

<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 8  
tttgcttcgt actcgggtcc t 21

<210> 9  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 9  
gcatcgcgat actagagaag 20

<210> 10  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 10

agcatcgaa tcggatccct aaaccaacgc caaagcccga at 42

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 11

tgatatgctg gagcttccct 20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 12

gcacaacctc ttccaggct 20

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 13

agcatcgat cctaacaatg tcaaacatgg caccactccc ta

42

[Brief description of the drawings]

[Figure 1]

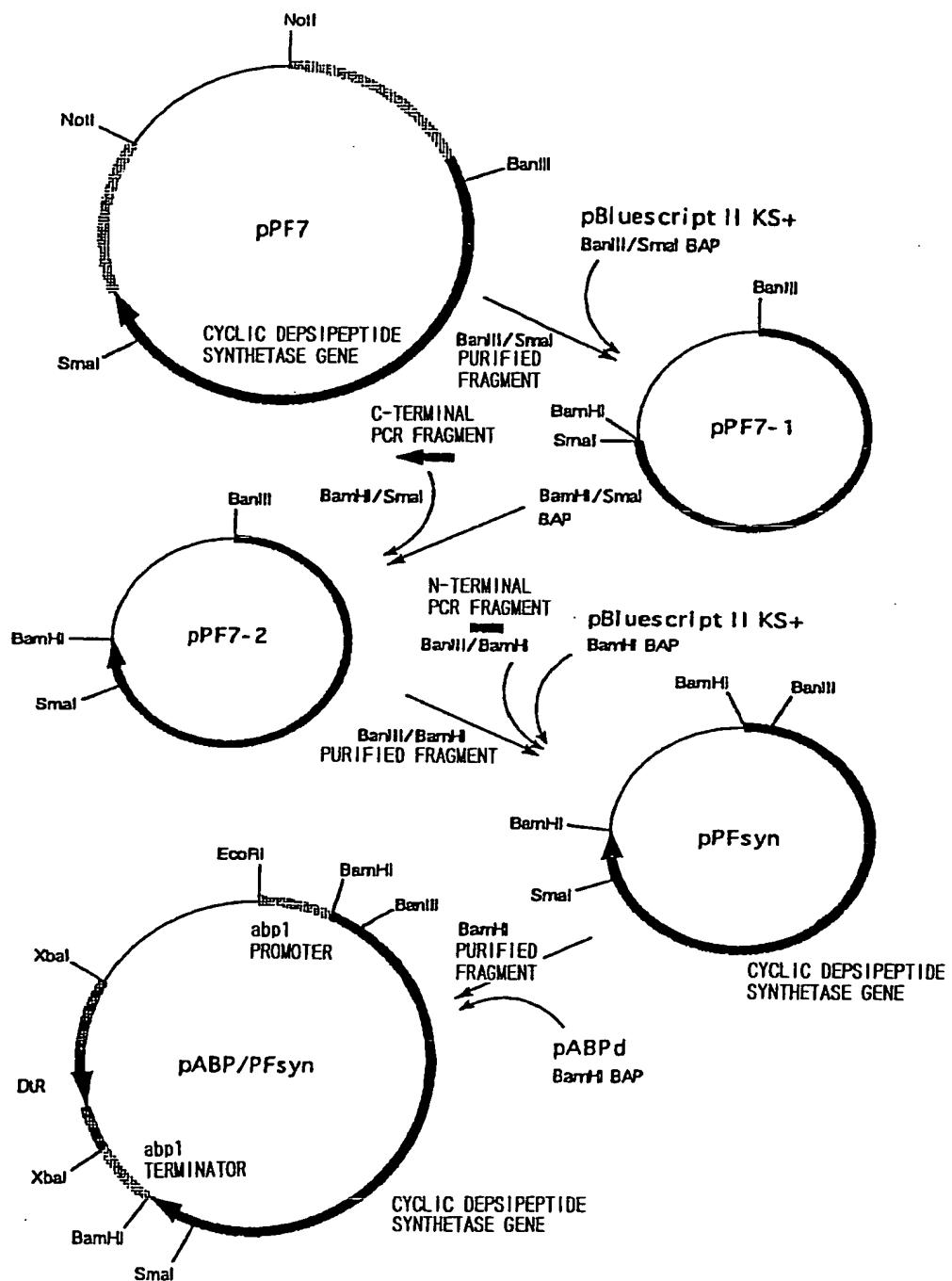
Figure 1 shows a construction procedure of plasmid pABP/PFsyn.

[Figure 2]

Figure 2 shows the results of electrophoresis of the proteins extracted from the parent strain and a gene-introduced strain into which pABP/PFsyn is introduced.

[Figure3]

Figure 3 shows the results of electrophoresis of the proteins extracted from the parent strain and a gene-introduced strain into which pABP/PFsynN is introduced.



# FIG. I



BEST AVAILABLE COPY

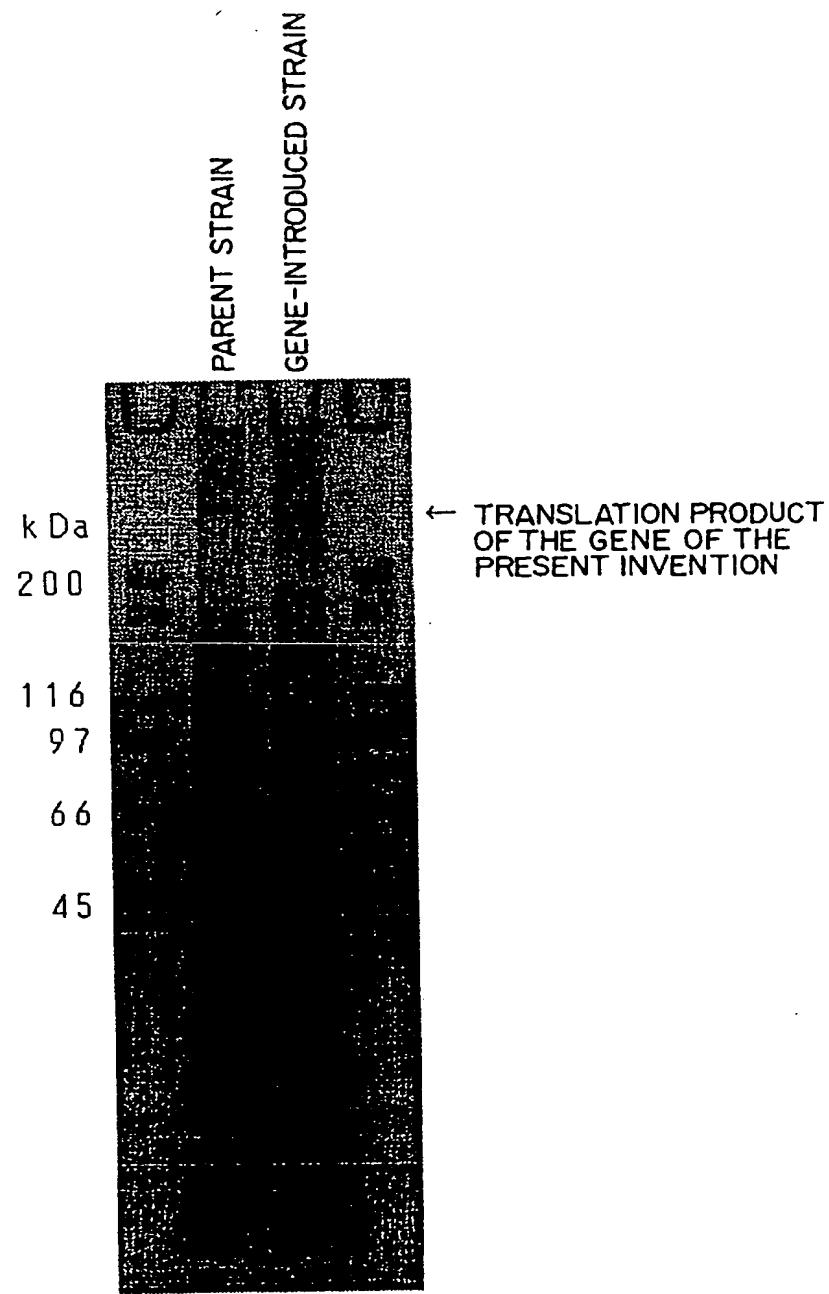


FIG. 2



BEST AVAILABLE COPY

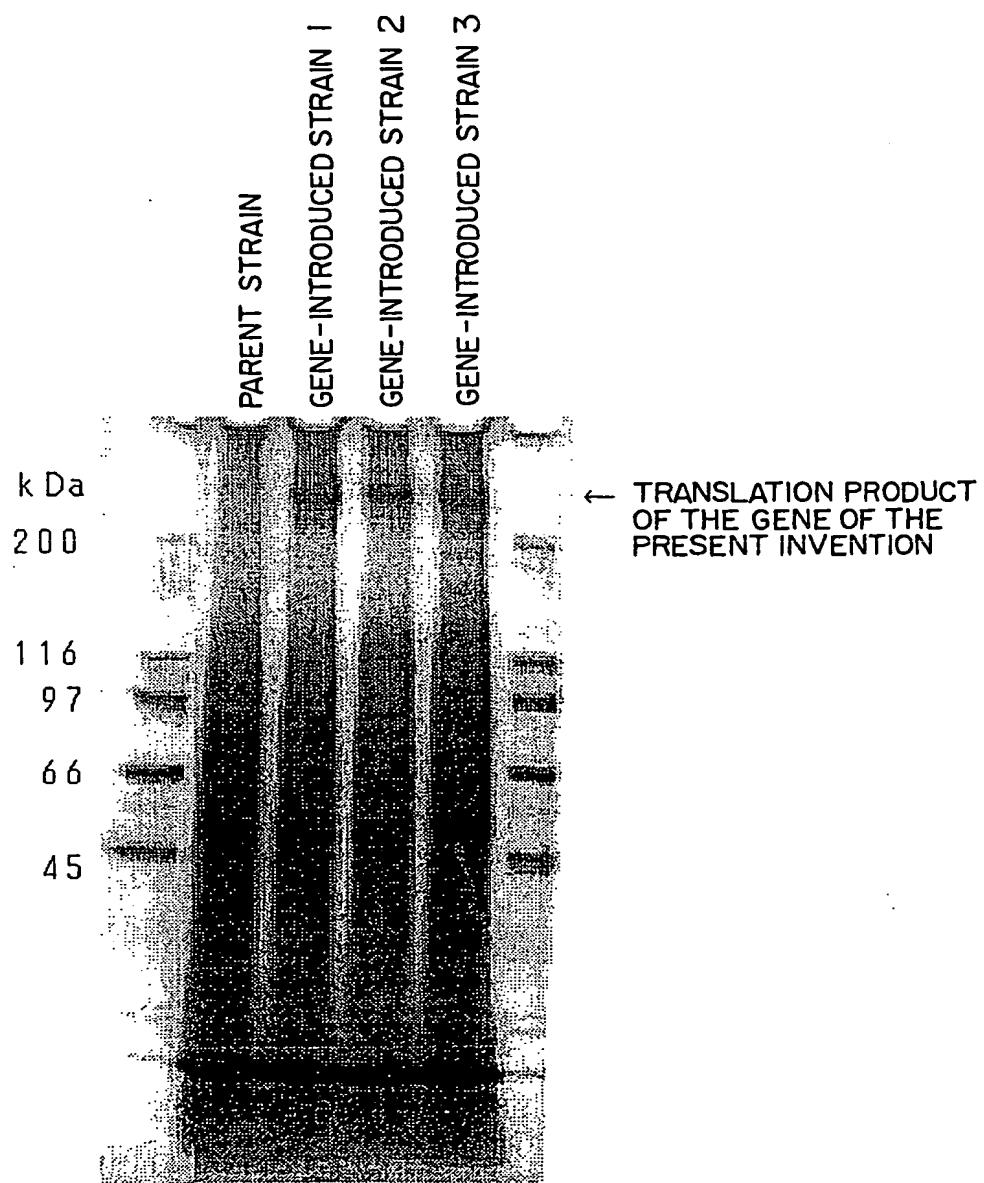


FIG. 3



[TITLE OF DOCUMENT] ABSTRACT

[ABSTRACT]

[OBJECT OF THE INVENTION]

To provide a method for producing a cyclic depsipeptide having anthelmintic activity, a cyclic depsipeptide synthetase gene capable of improving productivity of the substance PF1022 and a protein coding therefor, a recombinant vector comprising the gene, and a substance PF1022-producing microorganism and substance PF1022 into which the recombinant vector is introduced.

[MEANS FOR ATTAINING THE OBJECT]

A gene encoding a cyclic depsipeptide synthetase enhancing the biosynthesis of the substance PF1022 is isolated from a substance PF1022-producing microorganism. A recombinant vector is prepared by the substitution of the promoter and terminator of the gene with those of a foreign gene utilizable for expression augmentation, and then the recombinant vector is introduced into the substance PF1022-producing microorganism, whereby the improvement in productivity of the substance PF1022 was attained.

[SELECTED FIGURE]

None